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(without alignments)
1378.235 Million cell updates/sec
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3347
1 MSERKEGRGKGKKKERGS......QEEIQARLSSVIANQDPIAV 645
                                                                                                                          April 12, 2005, 14:21:26; Search time 181 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                  2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20028:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp20048:\*

A\_Geneseq\_16Dec04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2000s:\*

Database

## SUMMARIES

Description	Aay06635 Herugelin	Aab36793 Human her	Adb67619 Human her	Adn48871 Human her	Aar29571 Human her	Aay71172 Human Her	Human	Aay71198 Human Her	Human	Human	Aay71191 Human Her	Aay71182 Human Her	Aay71203 Human Her	Aay71194 Human Her	Aay71180 Human Her	Aay71185 Human Her	Aay71197 Human Her	Aay71186 Human Her	Aay71183 Human Her	Aay71190 Human Her	Aay71181 Human Her	Aay71187 Human Her	Aay71201 Human Her	Aay71184 Human Her	Aay71192 Human Her
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## ALIGNMENTS

RESULT 1

This sequence represents heregulin-beta-1 (HRG-beta-1) deduced from HRG-beta-1 cDNA (see AAX8701). The invention provides HRG ligands, including HRG-beta-1, that have affinity for and stimulate HRR2, HER3 and/or HER4 receptors in autophosphorylation. A new method of treating respiratory distress syndrome in humans uses HER2, HER3 and/or HER4 receptor ligands as epithelial growth factors. A novel method of inducing epithelial coll growth and/or proliferation comprises contacting a normal epithelial cell which expresses HER2, HER3 and/or HER4 receptors with an isolated ligand which extrates HER2, HER3, HER4 receptors or their combination. Also claimed are methods of increasing lung surfactant protein A, or of treating chronic obstructive pulmonary disease, respiratory distress or Heregulin-beta-1; HRG-alpha; human; ligand; HER2; HER3; HER4; receptor; Heregulin ligands can be used to induce epithelial cell growth, and to promote repair and healing of tissue damage or injury. distress syndrome; emphysema; Disclosure; Page 87-90; 120pp; English. AAY06635 standard; protein; 645 AA. lung surfactant; respiratory distre
epithelial growth factor; therapy. 98US-00020598. 99WO-US002390. (GETH ) GENENTECH INC. (IOWA ) UNIV IOWA RES FOUND. (first entry) Sliwkowski M, Kern JA; WPI; 1999-494213/41. Herugelin-beta-1. N-PSDB; AAX87701. Homo sapiens. W09939729-A2 03-FEB-1999; 04-FEB-1998; 26-OCT-1999 12-AUG-1999. AAY06635; AAYO6635

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The present invention relates to variants of heregulin that can bind to an BrbB receptor and include a portion of the 175-230 region of native human heregulin-betal. The variants may be used to promote ex vivo survival, proliferation and differentiation of cells, particularly when intended for transplantation. They may also be used to treat a wide range of cancers and diseases of the nervous system, musculature and epithelium
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llarity 100.0%; Pred. No. 2.2e-204;
Conservative 0; Mismatches 0;
                                                                                        Ballinger MD,
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     98US-00020880
                                97US-0037581P
                                                                                           WJ,
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                     DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                                                                   KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                            SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00097681,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0049492P.
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(GEOU ) UNIV GEORGETC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6727077-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a non-naturally occurring human epidermal growth factor receptor (HER)-3 variant polypeptide comprising amino acids 19-329 or 20-329 of the 1342 amino acid HER3 polypeptide (ABB67617) or a sequence which differs from native HER3 polypeptide and having amino acid substitutions at residues E43, N44, K51, E64, V66 and V110 of S1, is new. C substitutions at residues E43, N44, K51, E64, V66 and v110 of S1, is new. CC the variant HER-3 specifically binds to the heregulin polypeptide (ADB67619), or has an ability to inhibit the interaction between wild-type HER3 and heregulin. The polypeptide is useful for identifying a compound which specifically binds to heregulin binding constraint at HER3 variant polypeptide. The method further involves determining whether the test compound inhibits or enhances the heregulin condulates the interaction between a heregulin polypeptide. The polypeptide is also useful for wariant HER-3 polypeptide. The HER-3 polypeptide is also useful for condulates the interaction between a heregulin polypeptide and HER3 polypeptide, e.g. for treating cancer. The polypeptide is also useful for stimulating or activating HER3 receptor. This sequence represents the conduction between a heregulin polypeptide is also useful for stimulating or activating HER3 receptor. This sequence represents the conduction between a heregulin polypeptide is also useful for stimulating or activating HER3 receptor. This sequence represents the conduction between a heregulin polypeptide is also useful for conduction between a heregulin polypeptide is also useful for conduction between a heregulin polypeptide is also useful for conducting HER3 receptor. This sequence represents the conduction polypeptide.
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                                                                                                                                                                                   cytostatic; human epidermal growth factor receptor-3; HER-3; heregulin; HER2; tyrosine kinase activity; cancer.
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100.0%; Score 3347; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.2e-204;
Matches 645; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eisenberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 80; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Slamon DJ,
                                             ADB67619 standard; protein; 645 AA.
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                                                                                                                  (first entry)
                                                                                                                                                  Human heregulin protein.
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                           ADB67619
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/note= "deduced from ORF but initiating MET is at position 31 and the processed N-terminal residue
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08-NOV-1991;
06-MAR-1992;
11-MAY-1992;
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tor preparing a composition for diagnosing and treating cancer. The invention is also useful in gene therapy. The present sequence is human heregulin protein.
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                                                                                                                                      SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                                SEYSSIRFKWFKNGNEINRKNKPQNIKIQKKPGKSEIRINKASIADSGEYMCKVISKLGN
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                                                                                                             DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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                                                                                                                                                                                                              KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
                                                                                 Gaps
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                                                                645;
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                                                               Length
                                                                               Indels
                                                            Query Match 100.0%; Score 3347; DB 8; Best Local Similarity 100.0%; Pred. No. 2.2e-204; Matches 645; Conservative 0; Mismatches 0;
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(first entry)
                                           Sequence 645 AA;
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20-APR-1993
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Region
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Clone lambda heril.idbl (heregulin-beta-1) was identified in a lambda gill oligo-dT primed cDNA library derived from human breast carcinoma MDA 211 cells. Labelled synthetic DNA probes corresponding to the 5' and 3' ends of lambda heris (see AAQ11541) were used in the hybridisation reaction under high stringency conditions. The HRG-beta-1 clone extends 189 bp longer than lambda heris in the 3' direction and supplies a stop codon after Val 675. At nuclectide position 205 of lambda heril.idbl there is an A substituted for G which results in substitution of Gln in place of Arg at position 68 in HRG-beta-1. The other differences occur in the EGF metif of the two HRG proteins. See also AAQ31543-Q31548. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                         note= "serine-threonine potential O-glycosylation sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide(s) heregulin(s) bind the P185HER2 receptor - for diagnosing and treating tumours and screening for agonists or antagonists for binding to P185HER2.
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/note= "serine-glycine dipeptide potential glycosaminoglycan addition site - not part alpha sequence"
                                                                                                                                                                                          /note= "serine-glycine dipeptide potential glycosaminoglycan addition site"
                                                                                                              potential
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/note= "N-linked glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "N-linked glycosylation site"
                                                                                                           /note= "serine-glycine dipeptide glycosaminoglycan addition site"
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/note= "N-linked glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212. .251
/label= EGF motif
/note= "contains 6 cysteines"
278. .300
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'note= "probable"
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91US-00765212.
91US-00790801.
92US-00847743.
92US-00880917.
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                                                                                DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                                                                                                                    EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
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                                  1 MSERKEGRGKGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
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                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heregulin; HRG betal; human; hair cell; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome hair cell related hearing disorder; ototoxic injury; tissue damage; accoustic assault; degenerative hearing loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.

    .32
    'note= "Cleavage results in amino terminal fragment

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                 Indels
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        Pred. No. 2.3e-204;
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/label= Initiator_methionine
212. .251
                Mismatches
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100.08;
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                Conservative
      Similarity
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The patent discloses a method for inducing hair cell generation, or inner ear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HER2-10 medic receptors. Heregulin proteins function as activators of HER-2 oncogene and result from alternate splicing of a single gene mapped to chromosome 8p. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and coustic assault, degenerative hearing loss, balance impairments, damage associated with tissue damage, e.g. ottoxic injury, acoustic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders and heregulin, HRG-betal protein, derived from a genomic library. This sequence can be used to construct several variants
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                                          /note="Cleavage results in carboxy terminal fragment
HRG-betal protein"
261. .262
                                                                                                                                                                7076= "Cleavage results in carboxy terminal fragment HRG-betal protein"
276. 277
Anotes "Cleavage results in carboxy terminal fragment HRG-betal protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for inducing hair cell generation and inner-ear-supporting regeneration and proliferation, useful for treating hearing
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/label= Growth_factor_domain
/note= "HRG-beta-GFD"
255. .256
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                                                         Cleavage-site
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EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; heregulin; antiasthmatic; antiinflammatory; vulnerary; antiulcer; epithelial cell growth; HER2; HER4; HR64; HR05, lung cell; asthma; lung surfactant protein A; respiratory distress; emphysema; pneumonitis; chronic obstructive pulmonary disease; COPD; chronic bronchitis; ulcer; neconatal pulmonary disease; neonatal respiratory distress syndrome; emeconium aspiratory distress syndrome; acute lung injury; cystic fibrosis; surgical wound; resection; growth factor; smoke inhalation; HRG-betal.
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                                                                                                                                                                                                                                                                                           EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
                                                      PHHPNPPPERNVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
                                                                                                                                                                      RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                                                                                                                          511 RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEVETTQEYEPAQ
                                                                                                                                                                                                                                                                      EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIONPL
                              PHHPNPPPENVQLVNQYVSKXVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
                                                                                         SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                           SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRINGTGGPRECNSFLRHARETPDSY
                                                                                                                                                     RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                                                                                                 RPLILLVIPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing epithelial cell growth and/or proliferation, useful in the treatment of respiratory disease, comprises use of heregulin ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to inducing epithelial cell growth and/or proliferation comprising contacting a normal epithelial cell, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU09887 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human heregulin, HRG-betal
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N-PSDB; AAS18522.
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02-FEB-1999;
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corpresses HER2, HER3 and/or HER4 (preferably HER2/HER3, HER2/HER4, HER3 or HER4) receptors with an isolated ligand such as heregulin (HRG) which activates HER2, HER3 and/or HER4 receptors. The heregulin (HRG) which activates HER2, HER3 and/or HER4 receptors. The method is used for inducing epithelial call (preferably lung cell) growth and/or proliferation, for increasing lung surfactant protein A and for treating respiratory discress or emphysema, for treating chronic cobstructive pulmonary diseases including neonatal respiratory distress componical pulmonary diseases including neonatal respiratory distress componical diaphragmatic hernia and acute lung injuries including smoke or chemical inhalation, pneumonitis due to aspiration, near drowning, cystic fibrosis and other epithelial cell trauma diseases including injuries associated with surgical wounds and researcions, ulcers, lesions and tissue tears as normal epithelial cell growth factors. For tracting infants/neonates with respiratory distress as well as youth and adult with poor lung function due to lung injury or damage. The HRG binds with varying and very high affinity to the HER2, HER3 and/or HER4 receptors. The method stimulates growth and collinar barriers of organs and allowing the affected tissue to develop normal physiological functions more quickly. Hence the method improves collular barriers of organs and allowing the affected tissue to infection while treating lung cells that are damaged by inhalation of smoke resulting in emphysema. It also facilitates regeneration of epithelial cells. The Porce of human heregulin here, and the processing the affected of between the method improves the method sequence of human heregulin here.
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100.0%; Pred. No. 2.3e-204;
ive 0; Mismatches 0;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a method for inducing hair cell generation, or inner-
ear-supporting cell growth, regeneration, and/or proliferation, by
heregulins (HRG), the ligand for HRR2/HRR3 dimeric receptors. Heregulin
proteins function as activators of HER-2 oncogene and result from
alternate splicing of a single gene mapped to chromosome Bp. The two
major types, alpha and beta HRG's are based on two variant EGF-like
(epidermal growth factor) domains, that differ in their C-terminal ends.
This method can be used to increase the number of inner-ear-supporting
cells and for treatment of hair cell related hearing disorders and
disease states associated with tissue damage, e.g. octoxiz injury,
acoustic assault, degenerative hearing loss, balance impairments, damage
associated with surgery or physical injury and inner ear disorders
related to hair cell dysfunction. The present sequence is the human
heregulin ligand, HRG-betal protein variant-21. Note: This sequence is
not found in the specification and is derived from the HRG-betal protein
sequence found in Figure 2 (AAY71172)
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HRG-betal mature
                                                                                                                                                                                                                    Heregulin; HRG betal; human; mutant; mutein; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; ototoxic injury; tissue damage; acoustic assault; degenerative hearing loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for inducing hair cell generation and inner-ear-supporting ogrowth regeneration and proliferation, useful for treating hearing disorders.
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AASLEATPAFRLADSRINPAGRFSTQEEIQARLSSVIANQDPIAV
                  AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
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site corresponds to position 195, of the
protein, after initiatior Met (M11)"
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Human Heregulin HRG-betal protein variant-12.
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disorders.
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                                                                                                                                                                                                                                      Method for inducing hair cell generation and inner-ear-supporting ogrowth regeneration and proliferation, useful for treating hearing
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Pred. No. 3.6e-204;
1; Mismatches 0;
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                                                                                                           98US-0107522P.
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Matches 644; Conservative
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                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                        WPI; 2000-376313/32.
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              WO200027426-A1
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                                                                                                                                                   RPLILLVTPPRIREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                                                                                                                                                                                                  EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIONPL
                                                                                     RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                                                                                                                                         EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
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WPI; 2000-376313/32
                                                                       Misc-difference 230
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           Homo sapiens.
Synthetic.
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Pred. No. 3.6e-204;
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The patent discloses a method for inducing hair cell generation, or inner car-supporting cell growth, regeneration, and/or proliferation, by halfold the ligand for HERZ-HERS dimeric receptors. Hergulin proteins function as activators of HER-2 oncogene and result from a lternate splicing of a single gene mapped to chromosome Bp. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and disease states associated with tissue damage, e.g. octooxic injury, counstic assault, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human heregulin ligand, HRG-betal protein variant-14. Note: This sequence is note found in the specification and is derived from the HRG-betal protein sequence is noted.
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HRG-betal mature
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                                                                                                                           /note= "Wild type Lys replaced with Arg;
site corresponds to position 200, of the
protein, after initiatior Met (M31)"
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Pred. No. 3.6e-204;
                                                             label = Initiator methionine
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The patent discloses a method for inducing hair cell generation, or inner car-supporting cell growth, regeneration, and/or proliferation, by hergquins (HRG), the ligand for HRR2/HRR3 dimeric receptors. Heregulin proteins function as activators of HRR-2 oncogene and result from alternate splicing of a single gene mapped to chromosome 8p. The two major types, alpha and beta HRG's are based on two variant BGP-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cals and for treatment of hair cell related hearing disorders and disease states associated with tissue danage, e.g. ottoxic injury, counstic assault, degenerative hearing loss, balance impairments, damage related to hair cell dysfunction. The present sequence is the human related to hair cell dysfunction. The present sequence is the human related to hair eld dysfunction. The present sequence is the human related to hair eld dysfunction. The gresent sequence is the human related to hair eld dysfunction variant-5. Note: This sequence is not found in Figure 2 (AAY71172)
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Pred. No. 4.1e-204;
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the HRG-betal mature protein, after initiatior Met (M31
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                                                                                                                                                  KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVIASFYKHLGIEFMEA
                                                                                                                                                                                              EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
                                                                                                                                                                                                                                                                             PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
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                                                                                                                                                                                                                                                                                                                                                                SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                           KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heregulin; HRG betal; human; mutant; mutein; inner-ear-supporting ceactivator; HRR2 receptor; HER3 receptor; HER2 oncogene; chromosome hair cell related hearing disorder; ototoxic injury; tissue damage; accoustic assault; degenerative hearing loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Heregulin HRG-betal protein variant-17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses a method for inducing hair cell generation, or inner ear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HBR2/HBR3 dimeric receptors. Heregulin proteins function as activators of HBR-2 oncogene and result from alternate splicing of a single gene mapped to chromosome 8p. The two major types, alpha and bete HRG's are based on two variant BGP-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and disease states associated with tissue damage, e.g. ottoxic injury, associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human the specification and is derived from the HRG-betal protein or found in the specification and is derived from the HRG-betal protein contents.
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HRG-betal mature
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                                                                                                                        Heregulin; HRG betal; human, mutant; mutain; inner-ear-supporting cell; activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; ottochoxic injury; tissue damage; acoustic assault; degenerating loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
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site corresponds to position 226, of the
protein, after initiatior Met (M31)"
                                                                                   Human Heregulin HRG-betal protein variant-26.
                                                                                                                                                                                                                                                                                                                                                              /label= Initiator_methionine
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                         (first entry)
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les 644; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376313/32.
                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 256
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                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                       Homo sapiens.
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AAY71203;
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Matches
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Sequence 675 AA;
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                                                                                                                                                                                                              ear-supporting cell growth, regeneration, and/or proliferation, by heregulins (HRG), the ligand for HRS2/HER3 dimeric receptors. Heregulin proteins function as activators.of HER2/HER3 dimeric receptors. Heregulin alternate splicing of a single gene mapped to chromosome Bp. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear-supporting cells and for treatment of hair cell related hearing disorders and disease states associated with fissue damage, e.g. ototoxic injury, accoustic assoult, degenerative hearing loss, balance impairments, damage associated with surgery or physical injury and inner ear disorders related to hair cell dysfunction. The present sequence is the human regulin ligand, HRG-betal protein variant-17. Note: This sequence is not found in the specification and is derived from the HRG-betal protein sequence found in Figure 2 (AAY71172)
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                                                                                                                                                                                                  patent discloses a method for inducing hair cell generation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 4.1e-204;
0; Mismatches 1;
                                                                                                                                                                 English.
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Best Local Similarity 99.8%;
Matches 644; Conservative
                                                                                                                                                                 Disclosure; Page; 141pp;
(GETH ) GENENTECH INC.
                                                                 WPI; 2000-376313/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 675 AA;
                                                                                              Method for growth reg disorders.
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The patent discloses a method for inducing hair cell generation, or inner ear-supporting cell growth, regeneration, and/or proliferation, by hereafulins (HRG), the ligand for HRE2/HRE3 dimeric receptors. Heregulin proteins function as activators of HER-2 oncogene and result from a leterate splicing of a shiple gene mapped to chromosome 8p. The two major types, alpha and beta HRG's are based on two variant EGF-like (epidermal growth factor) domains, that differ in their C-terminal ends. This method can be used to increase the number of inner-ear supporting cells and for treatment of hair cell related hearing disorders and disease states associated with tissus damage, e.g. otocoxic injury, associated with surgery or physical injury and inner ear disorders can ented to hair cell dysfunction. The present sequence is the human heregulin ligand, HRG-betal protein variant-3. Note: This sequence is not found in Figure 2 (AAY71172)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Gln, Ile, Glu
/note= "This variable site corresponds to position 180 of
the HRG-betal mature protein, after initiatior Met (M31)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activator; HER2 receptor; HER3 receptor; HER-2 oncogene; chromosome 8p; hair cell related hearing disorder; otcoxxic injury; tissue damage; acoustic assault; degenerative hearing loss; balance impairment; treatment; surgical injury; physical injury; inner ear disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for inducing hair cell generation and inner-ear-supporting ogrowth regeneration and proliferation, useful for treating hearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner-ear-supporting
   AASLEATPAFRLADSRINPAGRFSTQEEIQARLSSVIANQDPIAV
                                        Heregulin; HRG betal; human; mutant; mutein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Heregulin HRG-betal protein variant-3
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                                                                                                                                                                                                                                                  AAY71180 standard; protein; 675 AA.
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99.9%; Score 3342; DB 3; Length 675; Similarity 99.8%; Pred. No. 4.8e-204; 4; Conservative 0; Mismatches 1; Indels 0; Gaps	MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS	MSERKEGRÜKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS	SEYSSLRFKWFKNGNELNRKNKPONIKIOKKPGKSELRINKASLADSGEYMCKVISKLGN	SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN	DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV	DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLX	KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA	KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA	EELYQKRVLTITGICIALLUVGIMCUVAXCKTKKQRKKLHDRLRQSLRSERNNMMIANG	BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG	PHHPNPPBENVQLVNQYVSKAVISSEHIVEREAETSFSTSHYTSTÄHHSTTVTQTPSHSW	PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW	SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY	SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRENUGTGGPRECNSFLRHARETPDDSY	RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEE	RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE	RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDBEEYETTQEYEPAQ	RPLLLLVTPPRLREKKFDHHPQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ	EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDËRVGEDTPFLGIQNPL	EPVKKLANSRRAKRIKFNIGHIANRLEVDSNISSOSSNSESETEDERVGEDTPFLGIQNPL	AASLEATPAFRLADSRINPAGRFSTQEELQARLSSVIANQDPIAV 645	AASLEATPAFRLADSRTNPAGRESTÕBEIGARLSSVIANODBIAV 675
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Search completed: April 12, 2005, 14:30:39 Job time : 183 secs

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9, Appli
                                                         April 12, 2005, 14:27:47 ; Search time 43 Seconds (without alignments) 1119.736 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-428-927-4
US-08-329-517-4
US-08-456-241-27
US-09-101-544-93
US-09-101-544-93
US-09-097-681-3
US-09-097-084295A-27
US-07-8477-743B-9
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US-08-467-602-270
US-08-411-295F-196
US-08-467-602-273
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US-08-411-295F-184
US-07-847-743B-28
US-08-456-201-28
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Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Patent No. 5367060

GENERAL INFORMATION:

APPLICANT Genentech, Inc.

TITLE OF INVENTION: Heregulin

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: EAGANALE FORM:
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA: 07/705256
FILING DATE: 24-May-1991
PRIOR APPLICATION DATA:
APPLICATION DATA: 07/705212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION DATA: 07/705212
FILING DATE: 08-No. 5367060-1991
ATTORNEY/AGBNT INFORMATION:
NAME: Hensley, MAX D.
         PCT-US92-04295A-28

US-08-467-602-274

US-08-467-602-264

US-08-411-295F-190

US-08-411-295F-190

US-08-411-295F-193

US-08-411-295F-193

US-08-467-602-267

US-08-411-295F-193

US-08-411-295F-193

US-08-411-295F-194

US-08-467-602-256

US-08-467-602-256
                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Heneley, Max D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 712
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 645 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inc
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Length 645;

100.0%; Score 3347; DB 1;

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US/08/126,145
                                      FILING DATE:
APPLICATION NUMBER: 07/880,917
PRIOR APPLICATION NUMBER: 07/705256
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/765212
APPLICATION NUMBER: 07/76901
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                27,034
ER: 712P4
                                                                                                                                                                 NAME: Heneley, Max D.
REGISTRATION NUMBER: 27,034
REFERENCE/DOCKET NUMBER: 712P-
TELECOMMUNICATION INFORMATION:
TELEPAN: 415/266-1489
TELERAX: 415/552-981
TELEX: 910/31-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               LENGTH: 645 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             Matches 645; Conservative
              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      US-08-456-201-27
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                                                            1 MSERKEGRGKGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
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                                        1 MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                                                                           KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
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                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.,
APPLICANT: Wandlen, Richard L.,
APPLICANT: Holmes, William E.
TITLE OF INVENTION: Structure, Production and Use of
TITLE OF INVENTION: Heregulin 2 Ligands
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEB: Genenech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
 Pred. No. 1.3e-244;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201
FILING DATE:
              0; Mismatches
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Patent No. 5641869
100.0%;
              645; Conservative
 Best Local Similarity
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US-08-456-201-27
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100.0%; Score 3347; DB 1; 100.0%; Pred. No. 1.3e-244;
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                                                       0; Mismatches
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481 RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEXETTQEYEPAQ 540
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                                 SUGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRINGTGGPRECUSFLRHARETPDSY
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APPLICANT: Ho, Wei-Heien
APPLICANT: Osheroff, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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21P: 94080-
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: 5.25 compatible
Compatible
PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
PILING DATE: 25-APR. 1995
CLASSIFICATION: 435
PRICH APPLICATION DATA:
PRICH APPLICATION DATA:
PRICH APPLICATION DATA:
PILING DATE: 14-NOV.1994
ATTORNEY/AGENT INPORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REGISTRATION NUMBER: 853D3
TELECOMMUNICATION:

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Patent No. 5756456
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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Matches 645; Conservative
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LENGTH: 645 amino aci
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US-08-428-927-4
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Pred. No. 1.3e-244;
O; Mismatches O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: 1BM FC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,926
FLING DATE: 25-APR-1995
CLASSIFICATION DATE: 25-APR-1995
FLING APPLICATION DATE: 35-APR-1995
FLING APPLICATION DATE: 18-NOV-1994
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       APPLICANT: Ho, Wei-Heien
APPLICANT: Oshercff, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
CONNTRY: USA
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REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853D4
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415/252-1994
TELEFAX: 415/952-9881
                                                                                                          Sequence 4, Application US/08428926
Patent No. 5667780
GENERAL INFORMATION:
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100.0%;
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 645; Conservative
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TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
APPLICANT: Obtarof, Phyllis L.
TITLE OF INVENTION: SENSORY AND MOTO
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: Generacch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08339517
Patent No. 5770567
   TELEFAX: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acide
                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 645; Conservative
                                                                                                      TOPOLOGY: linear
                                                                                                                    US-08-428-298-4
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US-08-339-517-4
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,298
FILING DATE: 25-APR-1995
CLASSIFICATION 19435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Galifornia
COUNTRY: USA
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| Patent No. 5762213
| GENERAL INFORMATION:
| APPLICANT: Ho, Wel-Hsien
| APPLICANT: Osheroff, Phyllis L.
| TITLE OF INFUNION: SENSORY AND MOS NUMBER OF SEQUENCES:
| CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853
TELECOMMUNICATION INFORMATION:
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US-08-428-298-4
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100.0%; Score 3347; DB 1;
100.0%; Pred. No. 1.3e-244;
iive 0; Mismatches 0;
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61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120
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                           601 AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
  601 AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.
APPLICANT: Holmes, William E.
TITLE OF INVENTION: STRUCTURE, PRODUCTION AND USE OF
TITLE OF INVENTION: HEREGULIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                 STREET: Genenceh, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: 112*
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,241
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
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APPLICATION DATA:
APPLICATION NUMBER: 08/126145
FILING DATE: 23-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880917
FILING DATE: 11-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/847743
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/75212
FILING DATE: 25-SEP-1991
PRIOR APPLICATION NUMBER: 07/75256
FILING DATE: 24-MAY-1991
APPLICATION NUMBER: 07/75256
FILING DATE: 24-MAY-1991
                                                                                                                                           Sequence 27, Application US/08456241
Patent No. 5840525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 00 REFERENCE/DOCKET NUMBER:
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amino acid
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Matches 645; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Pred. No. 1.
                                                                    COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,517
FILING DATE: 14-NOV-1994
CLASSIFICATION NUMBER: US/08/339,517
FILING DATE: ANOV-1994
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 053
TELECHOME: 415/225-1994
TELEFAX: 415/522-1994
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Best Local Similarity 100.
Matches 645; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
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COUNTRY:
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100.0%; Pred. No. 1.3e-244;
ive 0; Mismatches 0;
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APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Jones, Jennifer T.
APPLICANT: Fairbrother, Wayne J.
APPLICANT: Fliwkowski, Mark X.
APPLICANT: Wells, James A.
ITILE OF INVENTION: HEREGULIN VARIANTS
FILE REFERENCE: 14948-720CON2
CURRENT APPLICATION NUMBER: US 09/09/101,544
CURRENT APPLICATION NUMBER: US 09/020,880
PRIOR APPLICATION NUMBER: US 09/020,880
PRIOR FILING DATE: 1998-02-09
PRIOR PLING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-101-544-93
; Sequence 93, Application US/09101544
; Patent No. 638/638
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APPLICANT: Genetech, Inc.
APPLICANT: Genetech, Inc.
APPLICANT: Genetech, Inc.
APPLICANT: Ballinger, Marcus D.
APPLICANT: Jones, Jennifer T.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Sliwkowski, Mark X.
APPLICANT: Wells, James A.
TILE OF INVENTION: HEREGULIN VARIANTS
FILE REFERENCE: 14918-720CON1
CURRENT APPLICATION NUMBER: US/09/020,880A
CURRENT FILING DATE: 1997-02-19
SEARLIER FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 93
LENGTH: 645
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1×09-020-880-93
Sequence 93, Application US/09020880A
Patent No. 6136558
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US-09-020-880-93
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100.0%; Pred. No. 1.3e-244;
ive 0; Mismatches 0;
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FORTUGE 27, Application PC/TUS9204295A

Sequence 27, Application PC/TUS9204295A

GENERAL INFORMATION:
APPLICANT: Genemicch, Inc.
TITLE OF INVENTION: Berequin

TITLE OF INVENTION: Heregulin
                                       NAME: Hoover, Kenley K.
REGISTRATION NUMBER: 40,302
REFRENCE/DOCKET NUMBER: PF38:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-3098504
TELEFAX: 301-309-8439
                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: amino acids
  FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley K.
                                                                                                                                                                                                                                                                                                                                                                                 Matches 645; Conservative
                                                                                                                                                                                                                    TYPE: amino aciu
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: Hijazi, Mai
APPLICANT: Ruben, C. Richter
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Heregulin-Like Fac
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
CITY: No
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,681
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CLASSIFICATION:
PROR APPLICATION DATA:
APPLICATION NUMBER: US 60/049,942
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US-09-097-681-3
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Patent No. 5367060
GENERAL INFORMATION:
TITLE OF INVENTION: Structure, Production and Use;
TITLE OF INVENTION: Heregulin;
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITT: South San Francisco
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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SOFTWARE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
CLASSIPICATION: 424
PRIOR APPLICATION NATA:

APPLICATION NATA:

APPLICATION NUMBER: 07/765212
FILING DATE: 24-May-1991
PRIOR APPLICATION NUMBER: 07/765212
FILING DATE: 25-Sep-1991
FILING DATE: 26-Sep-1991
FILING DATE: 08-NO. 5367060-1991
ATTORNEY/AGENT INFORMATION:

NAME: Hensley, Max.

RESISTRATION NUMBER: 27,043
RESISTRATION NUMBER: 27,043
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TELEFAX: 415/952-9881
TELEX: 910/31-7168
INFORMATION FOR SEQ ID NO: 9:
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TYPE: AMINO ACID
TOPOLOGY: linear
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US-07-847-743B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEYSSIRFKWFKNGNEINRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SEYSSLRFKWFKNGNELNRKNKPONIKIOKKPGKSELRINKASLADSGEYMCKVISKLGN 120
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                                                                                                                                                                                                                      ZIP: 94050
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               COMPUTER: 15M C COMPUTER:
COMPUTER: 15M C COMPUTER:
COMPUTER: 15M C COMPUTER:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04295A
FILING DATE: 1992051
CLASSIFICATION:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
APPLICATION NUMBER: 07/765212
FILING DATE: 25-SEP-1991
APPLICATION NUMBER: 07/765212
FILING DATE: 25-SEP-1991
PRICA APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRICA APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
APPLICATION NUMBER: 07/790801
FILING DATE: 06-MAR-1992
ATTORNEY AGENT INFORMATION:
NAME: USERIAL OF THE 
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hensley, Max D.
REGIETRATION NUMBER: 27,043
REFRENCE/DOCKET NUMBER: 712P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/592-9881
TELEFRX: 415/592-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
NUMBER OF SEQUENCES: 30
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Best Local Similarity
Matches 645; Conserv
                                                                                                                                                                                                                  ZIP: 94080
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/705256
PRIOR APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                27,034
                                                                                                                                                                                                                                                                                        ATTORNET, TANSAN, TANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG 330
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                                    31 MSERKEGRGKGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
                                                                                                                               SEYSSLRFKWPKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
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MSERKEGRGKGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                                                                                                                                             DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.,
APPLICANT: Holmes, William E.;
TITLE OF INVENTION: Structure, Production and;
TITLE OF INVENTION: Heregulin 2 Ligands
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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US-08-456-201-9
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SEYSSIRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN 120 DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV 180 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLKQSLRSERNNMMIANG SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY 511 RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHV EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMANIANG 451 RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPVSSMTVSMPSMAVSPFMEEE RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDBEYETTQEYEPAQ **EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL** KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE 31 MSERKEGRGKGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS Gaps 0 732; Length 0; Indels AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV Query Match 100.0%; Score 3347; DB 1; Best Local Similarity 100.0%; Pred. No. 1.6e-244; Matches 645; Conservative 0; Mismatches 0;

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                                                    211 KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                       EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKTHDRLRQSLRSERNNMNIANG
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04295A
FILING DATE: 19920521
CLASSIFICATION:
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| GENERAL INFORMATION:
| TILLE OF INVENTION: Structure, Proc
| TITLE OF INVENTION: Heregulin | NUMBER OF SEQUENCES: 30 | CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc.
SYREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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APPLICATION NUMBER: 07/705256
PILING DATE: 24 MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
PILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
PILING DATE: 08-NOV-1991
PRIOR APPLICATION NUMBER: 07/790801
PRIOR APPLICATION NUMBER: 07/790801
PRIOR APPLICATION NUMBER: 07/847743
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 27,043
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OPERATING SYSTEM:
SOFTWARE: patin (
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PCT-US92-04295A-9
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Best Local Similarity 100.0%; Pred. No. 1.6e-244;
Matches 645; Conservative 0; Mismatches 0; Indels
                                                                                                                                 PRODUCTION AND USE OF
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPATER: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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FILING DATE: 31-MAY-1995
                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSITICATION 1943
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/126145
FILING DATE: 23-SEP-1993
PRICK APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 11-MAX-1992
PRILNG DATE: 11-MAX-1992
PRILNG DATE: 07/84743
PRILNG DATE: 07/847743
PRILNG DATE: 07/801
PRICK APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRILNG DATE: 28-SEP-1991
PRILNG DATE: 28-SEP-1991
PRILNG DATE: 28-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M:
                  ; Sequence 9, Application US/08456241; Patent No. 5840525; GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L. APPLICANT: Holmes, William E. TITLE OF INVENTION: STRUCTURE, PR. TITLE OF INVENTION: HEREGULIN NUMBER OF SEQUENCES: 30 CORRESPONDENCE ANDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1994
TELEFAX: 415/952-9881
TELEFAX: 910/311-7168
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 00,000
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US-08-456-241-9
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                                                                                                                                                                             Length 732;
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                                                                                                                                                                          Query Match 100.0%; Score 3347; DB 5; Best Local Similarity 100.0%; Pred. No. 1.6e-244; Matches 645; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: 712P;
TELEPHONE: 415/255-1994
TELEPAX: 415/952-981
TELERX: 910/371-7168
INPORMATION: FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 732 amino acids
TYPE: AMINO ACID
TOPOLOGY: 1inear
PCT-US92-04295A-9
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-I- MISCELLANEOUS: The sequence shown here is derived from an EMBL/Genbank/DDBA third party annotation (TPA) entry.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PSO0022; EGF 1; UNKNOWN 1.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50036; IG LIKE; 1.
SEQUENCE 645 AA; 71126 MW; 0487AFF528CDD628 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 3.3e-175;
1; Mismatches 1;
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(Q9EXA6
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(Q9ESA7
(Q9ESA7
(MRG3 MOUSE
NRG3 HUMAN
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SEQUENCE FROM N.A.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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9 9

Gaps

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Length 645; Indels

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9 9

Gaps

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300 292 360 352

420 412 480 472

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NRGI HUMAN STANDARD; PRT; 639 AA.

002297; 014667; P982022, 002299; Q071110; Q071111; Q12779;

Q12780; Q12781; Q12783; Q12783; Q12784; Q9UPE3;

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2004 (Rel. 45, Last amoutation update)

25-OCT-2004 (Rel. 45, Last amoutation update)

Pro-neuregulin-1 precursor (Pro-NRGI) [Contains: Neuregulin-1 (Neu differentiation factor) (Heregulin) (HRG) (Breast cancer cell differentiation factor p48) (Acetylcholine receptor inducing activity) (ARIA) (Sensory and motor neuron-derived factor) (Glial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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                                                                                                                                                                                                                                                                                                           0B89DF6E2ED70333 CRC64;
                                                                                                                                                                                                                                                                                                                                                               Score 3280; DB 2;
Pred. No. 4.4e-172;
1; Mismatches 1;
                                                                                                                                                                      PRINTS; PRO1089; NEUREGULIN.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS50026; EGF_3; 1.
PROSITE; PS50035; IG_LIKE; 1.
SECUENCE 637 AA; 70169 MW; 0889
      InterPro; IPR006209; EGF like.
InterPro; IPR007110; Ig-like.
InterPro; IPR002154; Neuregulin.
Pfam; PF00008; EGF; 1.
Pfam; PF00047; Ig; 1.
Pfam; PF02158; Neuregulin; 1.
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Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Sigurdsson E., Bryjolfsson J., Gunarsdottir S., Sigurdsson D., Gunarsdottir S., Ivanarsson O., Chou T.: Ghoaf S., Bryjolfsson J., Guntarsson H., Gudnadottir V.G., Gudmundsdottir E., Bjornsson A., Ingvarsson H., Ingason A., Sigfusson S., Hardardottir H., Harvey R.P., Brunner D., Mutel V., Gonzalo A., Lemke G., Sainz J., Johannesson G., Andresson T., Gudjartsson D., Manolescu A., Frigge M.L., Gurney M.E., Kong A., Gulcher J.R., Petursson H., Stefansson K.; "Neuregulin I and Susceptibility to Schizophrenia."; Am. J. Hum. Genet. 71:0-0(2002).

Figure S. M. M. S. M. S.
KCAEKEKTFCVNGGECFWVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                                                                                                      EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKKLHDRLRQSLRSERNNTWNIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHHPNPPPENVQLVNQVVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                                                                 BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRINGTGGPRECNSFLRHARETPDSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 EPVKKLANSRRAKRIKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
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Last annotation update)
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01-WAR-2004 (TrEWBLrel. 26, Created)
01-WAR-2004 (TrEWBLrel. 26, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last ann
Neuregulin 1 isoform HRG-beta2.
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Q12780; 1HRE.
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CHROMOSOMAL TRANSLOCATION.

MEDLINE=99455251; PubMed=10523851; DOI=10.1038/sj.onc.1202950;

Wang X.-Z., Jolicoeur B.M., Conte N., Chaffanet M., Zhang Y.,

Mozziconacci M.-J., Feiner H., Birnbaum D., Pebusque M.-J., Ron D.;

"Gamma-heregulin is the product of a chromosomal translocation fusing the DOC4 and HGL/NRG1 genes in the MDA-MB-175 breast cancer cell
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                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1; 6; 7 AND 8), AND PARTIAL SEQUENCE. MEDLINE=92271253; PubMed=130381; Holmes W.E., Sliwkowski M.X., Akita R.W., Henzel W.J., Lee J., Park J.W., Yansura D., Abadi N., Raab H., Lewis G.D., Shepard H.M., Kuang W.-J., Wood W.I., Goeddel D.V., Vandlen R.L.; "Identification of heregulin, a specific activator of p185erbB2."; Science 256:1205-1210(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=92208945; PubMed=1348215; DOI=10.1016/0092-8674(92)90131-U;
Peles E., Bacus S.S., Koski R.A., Lu H.S., Wen D., Ogden S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Breast cancer;
MEDLINE=97472144; PubMed=9333014; DOI=10.1038/sj.onc.1201317;
MEDLINE=97472144; PubMed=9333014; DOI=10.1038/sj.onc.1201317;
Schaefer G., Fitzpatrick V.D., Sliwkowski M.X.;
"Gamma-heregulin: a novel heregulin isoform that is an autocrine growth factor for the human breast cancer cell line, MDA-MB-175.";
Oncogene 15:1385-1394(1997).
                                                                                                                                                                                                                                                                                                                                                                                                 Wen D., Suggs S.V., Karunagaran D., Liu N., Cupples R.L., Luo Y., Anassen A.M., Ben-Baruch N., Trollinger D.B., Jacobsen V.L., Meng S.-Y. Lu H.S., Hu S., Chang D., Yang W., Yanigahara D., Koski R.A., Yarden Y., Structural and functional aspects of the multiplicity of Neu differentiation factors.";

Mol. Cell. Biol. 14:1909-1919(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93205115; PubMed=8096067; DOI=10.1038/362312a0;
Marchionni M.A., Goodearl A.D.J., Chen M.S., Bermingham-McDonogh (
Krk C., Hendricks M., Danehy F., Misumi D., Sudhalter J.,
Kobayashi K., Wroblewski D., Lynot C., Baldasarre M., Hiles I.,
Davis J.B., Hsuan J.J., Totty N.F., Otsu M., McBurney R.N.,
Waterfield M.D., Stroobant P., Gwynne D.;
"Glial growth factors are alternatively spliced erbB2 ligands
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-210 FROM N.A.
Schoumacher F., Herzer S., Flury N., Kueng W., Mueller H.,
Eppenberger U.;
                                                                            Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo, NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. OF GAMMA-HEREGULIN FUSION PROTEIN.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4; 6; 7 AND 8). 
TISSUE=Kidney adenocarcinoma, and Pituitary;
MEDLINE=94158863; PubMed=7509448;
                       Name=NRG1; Synonyms=GGF, HGL, HRGA, NDF, SMDF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
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MEDLINE=93366731; PubMed=7689552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 362:312-318(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 69:205-216(1992).
                                              (Human)
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                                           Homo sapiens
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Name=10; Synonyms=SMDF;

1sod=015491-1; Sequence=External;

1sod=015491-1; Sequence=External;

1rissus specificity: Type I isoform alpha is expressed in breast, ovary, testis, prostate, heart, skeletal muscle, lung, placenta liver, kidney, salivary gland, small intestine and brain, but not in uterus, stomach, pancreas, and spleen. Isoform 3 is the predominant form in mesenchymal cells and in nonneuronal organs, whereas isoform 5 is the major neuronal form. Isoform 8 is expressed in spinal cord and brain. Isoform 9 is the major form skeletal muscle cells; in the nervous system it is expressed in spinal cord and brain. Also detected in adult heart, placenta, lung, liver, kidney, and pancreas.

--- DEVELOPMENTAL STAGE: Detectable at early embryonic ages.
                                                                                                                                                                                                                                              MEDLINE-94341264; PubMed-8062836;
MAGGARE-94341264; PubMed-8062836;
MAGGARE-94341264; PubMed-8062836;
MAGGARE-94341264; PubMed-8062836;
MAGGARE-94341264; PubMed-8062836;
MAGGARE-94341264; PubMed-8062836;
MAGGARE-94341264; PubMed-806284;
MAGGARE-94164; A liagand for p180erbB-4.";
EMBO J. 133517-3523(1994).

I. FUNCTION: Direct ligand for ERBB3 and ERBB4 tyrosine kinase
receptors. Concomitantly recruits ERBB1 and ERBB2 coreceptors,
receptors. Concomitantly recruits ERBB1 and ERBB2 coreceptors,
resulting in ligand-stimulated tyrosine phosphorylation and
activation of the ERBB receptors. The multiple isoforms perform
diverse functions such as inducing growth and differentiation of
epithelial, glial, neuronal, and skeletal muscle cells; inducing
cypression of acetylcholine receptor in synaptic vessicles during
the formation of the neuromuscular junction; stimulating
lobuloalveolar budding and milk production in the mammary gland
and inducing differentiation of mammary tumor cells; stimulating
Schwann cell proliferation; implication in the development of the
myocardium such as trabeculation of the development of the
myocardium such as trabeculation of the development of the
myocardium such as trabeculation of the development of the
myocardium such as trabeculation of the development of the
myocardium such as trabeculation of the development of the
myocardium such as trabeculation of the development of the
myocardium such as trabeculation of an artive Implement and as a proteclytically released soluble growth factor form. The
membrane-bound form does not seem to be active. The secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing, Named isoforms=9;
Comment=Additional isoforms seem to exist. Isoforms have been classified as type I NRGs (isoforms with an Ig domain and a glycosylation domain, isoforms 19), type II NRGs (isoforms with an Ig domain but no glycosylation domain, isoform 9) and type II NRGs (isoform with a Cys-rich domain, isoform 10). All
                                                                          MEDLINE=20065180; PubMed=10597312; DOI=10.1038/sj.onc.1203136;
Liu X., Baker E., Eyre H.J., Sutherland G.R., Zhou M.;
"Gamma-heregulin: a fusion gene of DOC-4 and neuregulin-1 derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=8; Synonyms=Beta3, GGFHPB1;
IsoId=002297-8; Sequence=VSP 003429, VSP 003430;
Name=9; Synonyms=GGF2, GGFHPP2;
IsoId=002297-9; Sequence=VSP 003425, VSP 003426, VSP_003429,
VSP_003430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform 9 has a signal peptide. The isoform 8 may be nuclear ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  these isoforms perform distinct tissue-specific functions; Name=1; Synonyms=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=4; Synonyms=Alpha3;
IsoId=Q02297-4; Sequence=VSP_003432, VSP_003433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=3; Synonyms=Alpha2B;
IsoId=Q02297-3; Sequence=VSP_003434, VSP_003435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Teold=002297-1; Sequence=Displayed; Isold=002297-1; Sequence=VSP_003431; Isold=002297-2; Sequence=VSP_003431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=7; Synonyms=Beta2;
IsoId=Q02297-7; Sequence=VSP_003427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=6; Synonyms=Betal, BetalA;
IsoId=002297-6; Sequence=VSP_003428;
                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 175-241 (ISOFORM 1).
Oncogene 18:5718-5721 (1999).
                                                                                                                                                                             Oncogene 18:7110-7114 (1999)
                                                                                                                                                           chromosome translocation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGND 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVK 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQNQ----EKAE 235
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                                                                                                                                                                                                         -!- DISEASE Involved in a rare t (8;11) chromosomal translocation that fuses the 5'end of OD24 to NRG1 (isoform 8). The product of this translocation was first thought to be an alternatively spliced isoform, called gamma-heregulin. Gamma-heregulin is a soluble activating ligand for the ERBB2-ERBB3 receptor complex and acts as an autocrine growth factor in a specific breast cancer cell line (MDA-WB-175). Not detected in Dreast carcinoma samples, including ductal, lobular, medullary, and mucinous histological types, neither in other breast cancer cell lines.
-!- SIMILARITY: Belongs to the neuregulin family.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                           -!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By similarity).
                                                                            DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
DOMAIN: The cytoplasmic domain may be involved in the regulation
                                                                                                                PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                    of trafficking and proteolytic processing. Regulation of the proteolytic processing involves initial intracellular domain dimerization (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3193.5; DB 1
Pred. No. 2.5e-167;
2; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA19950.1; -.
AAA19951.1; -.
AAA19952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA19952.1; -.
AAA19953.1; -.
AAA19954.1; -.
AAA19955.1; -.
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AAA58640.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA58641.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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RA Stefansson H., Sigurdason E., Steinthorsdottir V., Bjornsdottir S., Sigmundason T., Ghosh S., Brynjolfsson J., Gunnarsdottir S., Sigmundason T., Ghosh S., Brynjolfsson J., Gunnarsdottir S., Jonsson H., Ra Ivarsson O., Chou T.T., Hjaltason O., Bigissdottir B., Jonsson H., Ra Ingason A., Sigfusson S., Hardardottir E., Bjornsson A., Ingvarsson B., Mutel V., Gonzalo A., Lewke G., Sainz J., Johannesson G., Andresson T., Gudpjattsson D., Manolecu A., Frigge M.L., Gurney M.E., Kong A., Gulcher J.R., Petursson H., Stefansson K.; Muteregulin I and Susceptibility to Schizophrenia."; M., J. Hum. Genet. 71:0-0(2002).

C. I. MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.

C. EMBL, BK000383; DAA0048.1; -...

C. GO:0005102; P:receptor binding; IEA.

G. GO:0005102; P:receptor binding; IEA.

DR GO: GO:000710; P:embryonic development; IEA.

InterPro; IPR007110; Ig-like.

DR Fam; PP00047; ig; 1.

PRESS. PROMESSEN INTERMENTATION: 19-11ke.

DR Fam; PP00047; ig; 1.
                                           481
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NGHTESILSESHSVIVMSSVENSRHSSPTGGPRGLNGTGGPRECNSFLRHARETPDSYR
                                                             DSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEER
                                                                                                                            PLLLVT PPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRI VEDEEYETTQEYEAQE
                                                                                                          PLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQE
                                                                                                                                                                       PVKKLANSRRAKRTKPNGHIANRLEVDSNTSSOSSNSESETEDERVGEDTPFLGIONPLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 640;
                                                                                                                                                                                                                                    ASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
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PROSITE; PSSONSS; IG LIKE; 1.
PROSITE; F40 AA; 70361 MW; 11AFC54B32527ACC CRC64;
                                                                                                                                                                                                                                                             ASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Neuregulin 1 isoform HRG-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.4%; Score 3192.5; DB 2 96.4%; Pred. No. 2.8e-167; ive 2; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                640 AA
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01089; NEUREGULIN.
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PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
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                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12145742;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=NRG1;
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241 BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRQKLHDRLRQSLRSERNNMVNIANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 SNGHTESIISESHSVIMMSSVENSRHSSPAGGPRGRLHGLGGPRECNSFLRHARETPDSY
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                                                                                                                                                                                                                                                                                                             61 SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                                                                                                                                                                                                             61 SEYSSLRFKWFKNGNELNRRNKPQNVKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
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P43322; P43323; P43325; P43325; P43327; P43328;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2004 (Rel. 44, Last annotation update)
Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: Neuregulin-1 (Neu differentiation factor) (Heregulin) (HRG) (Acetylcholine receptor inducing activity) (ARIA) (Sensory and motor neuron-derived factor)
                                                                                                                                                                                                                           ö
                                                                                                                                                                                               Length 645;
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                                                                                                                                                                   7E575AEF73F55047 CRC64;
                                                                                                                                                                                              94.1%; Score 3149; DB 2; 93.0%; Pred. No. 6.9e-165;
                                                                                                                                                                                                            ; Pred. No. 6.9e 21; Mismatches
           PÉAM; PF00008; EGF; 1.
PÉAM; PF00189; EGF; 1.
PÉAM; PF00189; Neuregulin; 1.
PRINTS; PR01089; NEUREGULIN.
SWART; SW00409; EG; 1.
SWART; SW00409; EGF; 1.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS50025; EGF 2; 1.
PROSITE; PS50835; IG_IKE; 1.
EGF-like domain.
SEQUENCE 645 AA; 71381 MW; 7E575A
 InterPro; IPR002154; Neuregulin.
                                                                                                                                                                                                                           Matches 600; Conservative
                                                                                                                                                                                                              Similarity
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                                        SEYSSLRFKWFKNGNEINRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                   DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                                                                                                                                                      EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANG
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                                                                                 DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
                           SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                                                                                                                                                                                             SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                                                                                                                                                                                                                                                                                    RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                       KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Wharyota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AASLEATPAFRLADSRTNPAGRFSTQEE1QARLSSVIANQDPIAV
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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PRINTS; PRO1089; NEUREGULIN.
SMART; SM00181; BGF; 1.
PROSITE; PS00022; BGF_1; 1.
PROSITE; PS01186; BGF_2; FALSE_NEG.
PROSITE; PS01186; BGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003598; Ig_c2.
InterPro; IPR002154; Neuregulin.
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InterPro; IPR006209; EGF_like.
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Pfam; PF02158; Neuregulin;
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InterPro; IPR006210; IEGF
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EMBL; U02321; AAA19946.1
EMBL; U02322; AAA19947.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U02323; AAA19948.1
EMBL; U02324; AAA19949.1
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HSSP, Q12780, 1HRE.
RGD, 621341, Nrgl.
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                                                                                                                     Name=Betal;
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  ***MEDLINE=98352096; PubMed=9685409; DOI=10.1074/jbc.273.32.20525;

***MEDLINE=98352096; PubMed=9685409; DOI=10.1074/jbc.273.32.20525;

***MEDLINE=98352096; PubMed=9685409; DOI=10.1074/jbc.273.32.20525;

***Tannamembrane neuregulins interact with LiM kinase 1, a cytoplasmic protein kinase implicated in development of visuospatial cognition.";

***Lannamembrane neuregulins interact 19980.**

***Lennamembrane neuregulins in REBB typosine kinase receptors. Concomitantly recruits ERBB1 and ERBB2 coreceptors. Concomitantly recruits ERBB1 and ERBB2 coreceptors. celling in ligand-stimulated tyrosine phosphorylation and activation of the ERBB receptors. The multiple isoforms perform diverse functions such as inducing growth and differentiation of epithelial, glial, neuronal, and skeletal muscle cells; inducing expression of acetylcholine receptor in synaptic vessicles during the formation of the neuromuscular junction; stimulating lobuloarveolar budding and milk production in the mammary gland and inducing differentiation of mammary tumor cells; stimulating myocardium such as trabeculation of the development of the entity of activation; implication in the development of the entity of activation.
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SUBCELULIAR LOCATION: Exists as a type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active.
ALTERNATIVE PRODUCTS:
                   Name=Nrgl; Synonyms=Ndf;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Neu differentiation factor: a transmembrane glycoprotein containing an EGF domain and an immunoglobulin homology unit."; Cell 69:559-572(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy R.B., Yarden Y., "Isolation of the neu/HER-2 stimulatory ligand: a 44 kd glycoprotein that induces differentiation of mammary tumor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92257596; Pubmed-1349853; DOI=10.1016/0092-8674(92)90456-M; Wen D., Peles E., Cupples R., Suggs S.V., Bacus S.S., Luo Y., Trail G., Hu S., Silbiger S.M., Levy R.B., Koski R.A., Lu H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 14-36.
MEDLINE-92208945; PubMed=1348215; DOI=10.1016/0092-8674(92)90131-U;
Peles E., Bacus S.S., Koski R.A., Lu H.S., Wen D., Ogden S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM ALPHA2C/NDF44), AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATION OF PROCESSING (ISOFORM ALPHA2C/NDF44).
MEDLINE=99069430; PubMed=8952099; DOI=10.1074/jbc.273.51.34335;
Liu X., Hwang H., Cao L., Wen D., Liu N., Graham R.M., Zhou M.;
"Release of the neuregulin functional polypeptide requires its cytoplasmic tail.";
                                                                                                                                                                                TISSUE=Fibroblast;
MEDLINE=9415863; PubMed=7509448;
Wen D., Suggs S.V., Karunagaran D., Liu N., Cupples R.L., Luo Janssen A.M., Ben-Baruch N., Trollinger D.B., Jacobsen V.L., Meng S.-Y., Lu H.S., Hu S., Chang D., Yang W., Yanigahara D., Koski R.A., Yarden Y., Chang D., Yang W., Yanigahara D., Structural and functional aspects of the multiplicity of Neu differentiation factors."
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Comment=Additional isoforms seem to exist;
Name=Beta4, Synonyms=NDF42A,
Isoid=P43322-1, Sequence=Displayed;
                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 273:34335-34340(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTION WITH LIMKL
(Glial growth factor)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 69:205-216(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fibroblast;
                                                                                                                NCBI_TaxID=10116;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                 Name=Beta1, Synonyms=NDF40;
Isold=P43322-5; Sequence=VSP_003437;
Name=Beta2, Synonyms=NDF40;
Isold=P43322-6, Sequence=VSP_003440, VSP_003441;
Name=Beta3, Synonyms=NDF2;
Isold=P43322-7; Sequence=VSP_003430, VSP_003439;
Isold=P43322-7; Sequence=VSP_003430, VSP_003439;
Isold=P43322-8; Sequence=VSP_003438, Sequence=VSP_003438, VSP_003438, VSP_00348, VSP_003438, VSP_003438, VSP_00348, V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: Extensive glycosylation precedes the proteolytic cleavage.-!- SIMILARITY: Belongs to the neurogulin family.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
IsoId=P43322-3; Sequence=VSP_003436, VSP_003443, VSP_003444;
                                                                                                                                                     VSP 003442;
                                                                                                                                    IsoId=P43322-4; Sequence=VSP_003436,
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PIR; I61718; I61718.
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462

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479
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      301 LRQSLRSERSNLVNIANGPHHPNPPPENVQLVNQYVSKNVISSEHIVEREVETSFSTSHY 360
                                                                                                                                              480 SMTVSMPSVAVSPFVEEERPLILVTPPRIREKKYDHHPQQLNSFHHNPAHQSTSLPPSPL
                                                                                                                                                                                                                                                                                                    540 RIVEDEEYETTQEYESVQEPVKKVTNSRRAKRTKPNGHIANRLEMDSNTSSVSSNSESET
                                                                                                                                                                                                                                                                                                                                                                               600 EDERVGEDTPFLGIQNPLAASLEVAPAFRLAESRTNPAGRFSTQEELQARLSSVIANQDP
                                                                 361 TSTAHKSTTVTQTPSHSWSNGHTESVISESNSVIMMSSVENGRRSSPAGGPRGRLHGLGG
                                                                                                                                                                                                     SMTVSMPSMAVSPFMEEERPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPL
                                                                                                                                                                                                                                                                              RIVEDBEYETTQEYEPAQEPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESET
                                                                                                                                                                                                                                                                                                                                                           EDERVGEDTPFLGIONPLAASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDP
                                            TSTAHHSTTVTQTPSHSWSNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGG
                                                                                                                     PRECNSFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P SEQUENCE FROM N.A.

Carcoll S.L., Sconecypher M.S., Anderson K.D., Pearson R.J. Carcoll S.L., Sconecypher M.S., Anderson K.D., Pearson R.J. Carcoll S.L., Sconecypher M.S., Anderson K.D., Pearson R.J. Or., A Frohnert P.W.;

Explain Frohmert P.W.;

LS SUBMITTER GOOT—1999 to the EMBL/GenBank/DDBJ databases.

LS SIMILARITY: Contains 1 ESF-like domain.

EMBL; AF194993; AAG28433.1; -.

EMBL; AF194993; AAG28433.1; -.

EMBL; AF194993; AAG28433.1; -.

EMBL; AF194993; AAG28433.1; -.

EMBL; AF194993; AAG2843.1; -.

EMBL; AF194993; AAG2843.1; -.

GO; GO:0009790; P:embryonic development; IEA.

R O; GO:0009790; P:embryonic development; IEA.

ENTEFPRO; IPR006219; EGF] i.

ENTEFPRO; IPR006219; EGF] i.

ENTEFPRO; IPR00710; Ig-like.

ENTEFPRO; IPR00710; Ig-like.

ENTEFPRO; IPR00716; IRR00716; IRR00716
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Last sequence update)
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PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1
EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
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SMART; SM00181; EGF; 1.
SMRT; SM002408; 1GC2; 1.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS50026; EGF 3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
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Q9ESA5
ID Q9ES<sup>2</sup>
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By similarity.

By similarity.

N-linked (GlCNAc. . .) (Potential).

N-linked (GlCNAc. . .) (Potential).

N-linked (GlCNAc. . .) (Potential).

PNETGDRCQUYVMASFYMTSRRKRGETEXFLERKLDHSLV
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-> HNLIAELRRNKAYRSKCMQIQLSATHLRPSSITHLGFI
L (in isoform Alpha2B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                                                                                                                                                                                                                                                                                      KES -- QPGFTGARCTENVPMKVQTQE (in isoform Alpha2A, isoform Alpha2B and isoform Alpha2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTSRRKRÖETEKFLERKIDHSLVKESK -> KHLGIEFME (in isoform Betal). /FTId=VSP 003437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSERKEGRGKGKKKKDRGSRGKPGPAEGDPSPALPPRLKEMKSQESAAGSKLVLRCETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KHLGIEFWEAEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDR
                      protein sequencing; EGF-like domain;
Immunoglobulin domain; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFY-----
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                                                                                                 .neuregulin-1, membrane-bound form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (In isoform Beta2 and isoform
                                                                                                                                                      Internal signal sequence (Potential).
Cytoplasmic (Potential).
Ig-like C2-type.
SGF/Thr-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTIG=VSP 003440.
PPENVQ -> RVRTRG (in isoform Beta2)
/FTIG=VSP_003441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform Beta3)
/FTId=VSP_003439.
                                                                                                 Pro-neuregulin-1, membran
Neuregulin-1.
Extracellular (Potential)
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91.4%; Score 3058.5; DB 1
Best Local Similarity 89.1%; Pred. No. 6.7e-160;
Matches 591; Conservative 25; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       003442.
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PS50835; IG_LIKE; 1. ive splicing; Direct pein; Growth factor;
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                    Alternative spl
Glycoprotein; G
Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
STRANSWHIED LEGIONARY TISSUE—Brain,
MEDLINE—93201602; bubMed=8453670; DOI=10.1016/0092-8674(93)90407-H;
Falls D.L., Rosen K.M., Corfas G., Lane W.S., Fischbach G.D.;
"ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member of the neu ligand family.";
                                                                                            SEYSSLRFKWFKNGNELNRKNKPENIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                                    KCAEKEKTFCVNGGECFTVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                          EELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIANG
                                                                                                                                                                                                                      PHHPNPPPENVOLVNOYVSKNVISSEHIVEREVETSFSTSHYTSTAHHSTTVTOTPSHSW
                                                                                                                                                                                                                                                                                                     SNGHTESVISESNSVIMMSSVENSRHSSPAGGPRGRLHGLGGBRD-NSFLRHARETPDSY
                                                                                                                                                                                                                                                                                                                                              558 RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSVAVSPFVEEE
                                                                                                                                                                                                                                                                                                                                                                                    EPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPL
                                                                                                                                                                                                                                                                                                                                                                                                                             EPVKKYTNSRRAKRTKPNGHIANRLEMDSNTSSVSSNSESETEDERVGEDTPFLGIQNPL
                                                            139 SGRAPPAFRASFPPLETGRNLKKEVSRVLCKRCALPPRLKEMKSOESAAGSKLVLRCETS
                                                                               SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN
                                                                                                                        DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV
                                                                                                                                                                 KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEA
                                                                                                                                                                                                                                                                                         SNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSY
                                                                                                                                                                                                                                                                                                                                  RDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEE
                                                                                                                                                                                                                                                                                                                                                                          RPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      varius garius (viitoriu).
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                     Gaps
                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuregulin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV 645
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRG1 CHICK STANDARD; PRT; 602 AA. 005199; 073750; 073751; 073752; 16-0CT-2001 (Rel. 40, Last sequence update) 65-JUL-2004 (Rel. 44, Last annotation update) Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: New (Accetylcholine receptor inducing activity) (ARIA)].
. 16-156;
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4)
          Š.
          Pred.
                    23;
         89.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=NRG1; Synonyms=ARIA;
Gallus gallus (Chicken)
Eukaryota; Metazoa; Chorda
                    579; Conservative
                                       SGKKPESAAGSOSP-
        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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                                                                                                                                                              symptogenesis.".

Neuron 20.255-270(1998).

-I-FUNCTION: Direct ligand for the ERBB tyrosine kinase receptors.

The multiple isoforms perform diverse functions: cysteine-rich domain containing isoforms (isoforms 2-4) probably regulate the expression of nicotinic acetylcholine receptors at developing interneuronal synapses. The Ig-MRG isoform is required for the initial induction and/or maintenance of the mature levels of acetylcholine receptors at neuromuscular synapses.

-I-SUBCELLULAR LOCATION: Exists as a type I membrane protechytically released soluble growth factor form. The membrane-bound form does not seem to be active (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extensive glycosylation precedes the proteolytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ED4) in both visceral and somatic motor neurons of spinal cord and is highest at ED6. Isoform 1 is not expressed until ED 6 in spinal cord. At ED 11 both isoforms display comparable levels. DOMAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing. Regulation of the proteology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoid=Q05199-4; Sequence=VSP 003445, VSP 003446, VSP 003447, VSP 003448; Note=The EGF-like domain is replaced by a cysteine-rich domain
                                DOI=10.1016/S0896-6273(00)80454-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by a cysteine-rich domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSP_003446;
by a cysteine-rich domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: Isoforms 2-4 are detected at embryonic day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Extensive glycosylation precedes the proteolytic cleaves almilarity).
SIMILARITY: Belongs to the neuregulin family.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                 of
                                                             Yang X., Kuo Y., Devay P., Yu C., Role L.; "A cysteine-rich isoform of neuregulin controls the level expression of neuronal nicotinic receptor channels during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note=Contains an Ig-like domain;
Name=2; Synonyme=CRD-NRG-BETAIA,
IsoId=005199-2; Sequence=VSP_03445;
Note=The EGF-like domain is replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=3; Synonyms=CRD-NRG-BETA2A;
IsoId=Q05199-3; Sequence=VSP 003445,
Note=The EGF-like domain is replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1; Synonyms=ARIA, IG-NRG;
IsoId=Q05199-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synonyms=CRD-NRG-BETA2B;
TISSUE=Brain, and Spinal cord;
MEDLINE=98150951; PubMed=9491987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dimerization (By similarity).
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EGF like.
IEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000742;
InterPro; IPR006209;
InterPro; IPR006210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR007110;
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EMBL;
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SISTSTIGISHLVKCAEKEKTFCVNGGECPMVKDLSNPSRYLCKCPNEFIGDRCQNYVMA 227
                                                                                                                                                                                                                                                                                                                                                  SFYKHLGIEFMEAEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKORKKLHDRLRQSL 287
     SRHTSPT-GPRGRLNGIGGPREGNSFLRHARETPDSYRDSPHSERYVSAMTTPARMSPVD 401
                                                                                                                                                                                                                                                                                                                       SSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQEPVKKLANSRRAKRTKPNGHIAN 563
                                                                                                                                                                                                                                                                                                                                                                                                                                    RLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNPLAASLEATPAFRLADSRTNPAGRF 623
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                                                                                                                                                                                                                                        STSTSTTGTSHLIKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charton B.S., Ghashghaei H.T., Weber J.L., McCann C., Fischer T.M., Cheung I.D., Gassmann M., Messing A., Klein R., Schwab M.H.,
Lloyd K.C., Lal C.;
Lud C.;
L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinge; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Neuregulin-1 type III betal-a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STOREIGARLSSVIANODPIAV 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Nrg1;
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                                                                                                                                                                                                                                                                                                                                                                                           Neuregulin-1.

Extracellular (Potential).

Internal signal sequence (Potential).

Cytoplasmic (Potential).

Ig-like C2-type.

Ser/Thr-rich.

EGF-like.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlCNAC. . .) (Potential).

N-LINKEG (GLCNAC. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANGPHHPNPPPENVQLVNQYVSKNVI 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 SSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESILSESHSVIVMSSVEN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSRPFLQPSLYNRILDVGLWSSATPSLSPSSLEPTTASQAQ
ATETNLQTAPKLS (in isoform 2, isoform 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 EGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFCVNGGECFMVKDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 ESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEYSSLRFKWFKNGNELNRKNKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_003446.
VSAMTTPARMSPVDFHTP -> HTPPTSLLLAGKVSLRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPSRYLCKCPNEFTGDRCQNYVMASFYKHLGI EFMEAEELYQKRVLTITGICIALLVVGI
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                                                                                     Pfam; PF02158; Neureywarn; PR10189; Neureywarn; PR10189; Neuregulin.
PR10189; NeUREGULIN.
SWART; SW00181; EGF; 1.
SWART; SW00122; EGF 1; 1.
PROSITE; PS01186; EGF2; FALSE_NEG.
PROSITE; PS01186; EGF2; FALSE_NEG.
PROSITE; PS0835; IG_LIKE; 1.
Alternative splicing; Direct protein sequencing; EGF-like domain; Alternative splicing; Direct protein; Growth factor; Immunoglobulin domain; Transmembrane.

1 602
Pro-neuregulin-1, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (In isoform 3 and isoform 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.5%; Score 2526.5; DB 1; Length Best Local Similarity 77.2%; Pred. No. 9.7e-131; Matches 480; Conservative 54; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (In isoform 4). /FIId=VSP_003448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       003445.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR002154; Neuregulin.
Pfam; PF00047; ig; 1.
Pfam; PF02158; Neuregulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602 AA; 67453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405
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                                                                                                                                                                                                                                                                                                                                  380 SVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDSYRDSPHSERYVSAMTTPARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 SPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEEERPLLLVTPPRLREKKFDHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 PQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQEPVKKLANSRRAKRTKPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 HIANRLEYDSNISSQSSNSBSETEDERVGEDTPFLGIQNPLAASLEATPAFRLADSRTNP
196 ARTPEVRTPKSGTQPQTTETNLQTAPKLSTSTSTTGTSHLIKCAEKEKTFCVNGGECFTV
                                                          KDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEELYQKRVLTITGICIALL
                                                                                             260 VVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANGPHHPNPPPENVQLVNQYVS
                                                                                                                                                                                                                                                                                                   KNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESILSESHSVIVMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BDIX;
Carroll S.L., Anderson K.D., Frohnert P.W.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 EGF-like domain.
EMBL; AF194439; AAG28428.1; --...
HSSP; Q12780; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5277F2CBA2FB6878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
SMDF neuregulin alpha 2a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO, GO:0005102; F:receptor binding; IEA.
GO, GO:0009700; F:receptor binding; IEA.
GO, GO:0009700; P:embryonic development; IEA.
InterPro; IPR000742; EGF 2.
InterPro; IPR0002109; EGF 1ike.
InterPro; IPR002114; HPr_SerP_S.
InterPro; IPR002114; HPr_SerP_S.
InterPro; IPR002154; Neuregulin.
Pfam; PF00108; EGF; 1.
PRMTS; PR01089; Neuregulin; 1.
PRMTS; PR01089; Neuregulin; 1.
PRMTS; PR01089; Neuregulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
EGF-11; PS00589; PTS_HPR_SER; UNKNOWN_1.
EGF-11; COMMIN.
SEQUENCE 695 AA; 75646 MW; 5277F2CBA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620 AGRESTQEEIQARLSSVIANODPIAV 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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SEQUENCE FROM N.A.
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                                              343 RSERNIMWNIANGPHHPNPPPENVQLVNQYVSKNVISSEHIVEREVETSFSTSHYTSTAH
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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C STRAIN=Sprague-Dawley;
C STRAIN=Sprague-Dawley;
C STRAIN=Sprague-Dawley;
L Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
1 SIMILARITY: Contains 1 EGF-like domain.
EMBL; AF194189; AAG28427.1; -.
EMBL; AF19780; LHFE.

GO; GO:0005102; F:receptor binding; IEA.

GO; GO:0009790; Pembryonic development; IEA.

R InterPro; IPR006210; EGF-2.
R InterPro; IPR006210; EGF-1; ESF-S.
R InterPro; IPR006210; EGF-1; ESF-S.
R InterPro; IPR006210; IEGF-1.
R FORDIS PRO189; Neuregulin.
PFRAINTS; PR01089; NEUREGULIN.
SMART; SM01081; EGF-1.
R PROSITE; PS00022; EGF-1; UNIXNOWN-1.
R PROSITE; PS00022; EGF-1; UNIXNOWN-1.
R PROSITE; PS000289; PTS_HPR_SER; UNIXNOWN-1.
R PROSITE; PS000589; PTS_HPR_SER; UNIXNOWN-1.
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Last sequence update)
Last annotation update)
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Best Local Simil
Matches 456; C
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                                                                                                             SGEYMCKVISKLGNDSASANITIVESNEIITGMPAS--TEGAYVSS------ESP
                                                                                                                                                                  SSEAYTSPVSK-AQSEAGAHVTVQGDHAAVASEPSAVPTRKNRLSAFPPFHPTAPPFPSP
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MEDLINE=98352126; PubMed=968585; DOI=10.1016/S0169-328X(98)00085-0;
Yang J.F., Zhou H., Pun S., Ip N.Y., Peng H.B., Teim K.W.K.;
"Cloning of CDNAs encoding xenopus neuregulin: expression in myotomal muscle during embryo development.";
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MEDLINE=99316087; PubMed=10383827; DOI=10.1006/mcne.1999.0759;
Yang J.F., Zhou H., Choi R.C., Ip N.Y., Peng H.B., Tsim K.W.K.;
M.A Cysteine-rich form of Xenopus neuregulin induces the expression of acetylcholine receptors in cultured myotubes.";
                                                          Gaps
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-UJL-2004 (Rel. 44, Last annotation update)
Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: Neuregulin-1]
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleost
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
  Length 695;
                                                       Indels
Score 2211; DB 2;
Pred. No. 2.5e-113;
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                                                  Conservative 33; Mismatches
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66.1%;
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                          Similarity
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF076618; AAC26804.1; -.

R HASP; Q12780; IHRE.

R INTERPO; IPR000742; EGF 2.

R InterPro; IPR000509; EGF like.

R InterPro; IPR000110; Ig-like.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR00110; Ig-like.

R Pfam; PF00189; Weuregulin.

R Pfam; PR0189; Neuregulin; 1.

R PRIMTS; PR01089; Neuregulin; 1.

R PRIMTS; PR01089; Neuregulin; 1.

R PROSITE; PS00022; EGF 1; 1.

R PROSITE; PS0026; EGF 3; 1.

R PROSITE; PS0038; IG-like; 1.

R PROSITE; PS0038; IG-like; Gomain; Glycoprotein; Growth factor;
Mol. Cell. Neurosci. 13:415-429(1999).

-i- FUNCTION: Direct ligand for the ERBB tyrosine kinase receptors.

Induces expression of acetylcholine receptor in synaptic nuclei.

-i- SUBCELLULAR LOCATION: Exists as a type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By
                                                                                                                                                                                                             Name=CRD; Synonyms=CRD-NRGI, Cybreine-rich domain;
Isold=093183-2; Sequence-VSP 003449, VSP 003450;
TISSUE SPECIFICITY: Isoform alphal is expressed in brain and muscle. Isoform CRD is expressed in brain and spinal cord, but at very low level in muscle.

DEVELOPMENTAL STAGE: Strong expression in developing brain and spinal cord of the embryo. Also expressed in the myotomal muscle. DOMAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing. Regulation of the proteolytic processing involves initial intracellular domain
                                                                                                                                           isoforms seem to exist. Isoforms have alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similative, y, control but a standard but a signal sequence (Potential).

Cytoplasmic (Potential).

Ig-like C2-type.

Ig-like.

By similarity.

By similarity.

By similarity.

By similarity.

No similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuregulin-1 (By similarity).
Pro-neuregulin-1, membrane-bound form
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
--- SIMILARITY: Belongs to the neuregulin family.
--- SIMILARITY: Contains 1 EGF-like domain.
--- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                           Event=Alternative splicing, Named isoforms=2;
Comment=Additional isoforms seem to exist.
                                                                                                                                                                                            IsoId=093383-1; Sequence=Displayed;
                                                                                                                                                               or beta-type EGF-like domains;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                             (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain;
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280
677
677
233
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37
37
188
192
200
222
124
                                                                                                                                                                                 Name=Alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin
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CARBOHYD
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                                                                                                                                                                                                                       CETSSEYSSLRFKWFKNGNELNRKN----KPQNIKIQKKPGKSELRINKASLADSGEYMC 112
                                                                                                                                                                                                                                                             KVISKLGNDSASANITIVES---NEI-----ITGMPASTEGA---YVSSESPIRISV 158
                                                                                                                                                                                                                                                                                                                                                         ARCTETDPLRVVRS-EKHLGIEFMEAEELYQKRVLTITGICIDLLVVGDMCVVDAYCKTK 287
                                                                                                                                                                                   26
                                                                                                                                                                                                     26
         MAEKKKVKEGKGRKGKGKKDRKGKKAEGSDGGAASPKLKE
INTQSVQEGKLJVLKCQAVSEQPSLKFRWFKGEKELGAKNK
PDSNFEHTKLRGKKSSELDISKASSADNGEYKCMVSNQLG
NDTVTVNVTIVVK -> MSEDTAEGLONGCSEQSSDPPSAE
                                               LQNEESMPETQDEEETTHGITGLAITCCVCLEADRLRICLN
SEKICIIPILACLISLCLCIAGLKWVFVDKIFEYDSPTHLD
                                                                 PGHRQDLILYTDTAPSTLVPSSVRTLPVIIPTTDSKAAVT
FKFGTSLLPTE (in isoform CRD).
/FTId=VSP.003449.
                                                                                                -> PNEFTGD
                                                                                                                                                                                            1 MSER---KEGRG-KGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLR
                                                                                                                                                                                                                                  177 TKRG------DITAGPGHLIKCSDKEKTYCVNGGECYVLNGITSSNOFMCKCKPGFTG
                                                                                                                                                                                                                                                                                                                                                                            KORKKLHDRLRQSLRSBRNNMMNIANGPHHP-NPPP-ENVOLVNQYVSKNVISSEHIVER
                                                                                                                                                                                                                                                                                                                                                                                       EAETSFSTSHYTSTAHHSTTVTQTPSHSWSNGHTESILSE-SHSVIVMSSVENSRHSSPT
                                                                                                                                                                                                                                                                                                                                                                                                                              ETETSFSTSHYTSTTHHSTTVTQTPSHSWSNGLSESMISEKSYSVIVTSSVENSRHTSPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GPRGRINGIGGPRDC-SYLRHARDTPDSYRDSPHSERYVSAMTTPARMSPVEFKTPISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSPPSEMSPPVSSMTVSMPSMAVSPFMEEERPLLLVTPPRLREKKFDHH-PQ-----QFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEGANTSSSTSTSTTGTSHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTG
                                                                                                                                                                                                                                                                                                                                       DRCQN----YVMASFYKHLGIEFMEABELYQKRVLTITGICIALLVVGIMCVV-AYCKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPAQEPVKKLANSRRAKRIKPNGHIANR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                52;
                                                                                                                                            62.8%; Score 2102; DB 1; Length 677; 64.1%; Pred. No. 2.3e-107;
                                                                                             KPGFTGARCTETDPLRVVRSEKHLGIEFME
RCQNYVMASFYK (in isoform CRD).
/FTId=VSP_003450.
                                                                                                                                                               Indels
                                                                                                                          49279E8F5BAE396F CRC64;
                                                                                                                                                                86; Mismatches 105;
                                                                                                                          75794 MW;
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TQEELQARLSS-IANQ 660
                                                                                                                                                                Conservative
 130
                                                                                                                          AA;
                                                                                                                                                     Best Local Similarity
Matches 433; Conserv
                                                                                              223
                                                                                                                          677
CARBOHYD
VARSPLIC
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462 AA

Q7RTW1 PRELIMINARY; PKT; Q7RTW1; 01-MAR-2004 (TrEMBLrel. 26, Created)

RESULT 13 Q7RTW1

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                                                                                                                                                                                                                                                                                                                                                          A Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., A Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Sigmundsson T., Ghosh S., Brynjolfsson J., Gunnarsdottir S., A Ingason T., Ghosh S., Brynjolfsson J., Gunnarsdottir S., A Ingason T., Ghosh S., Hailteson O., Blornsson A., Ingvarsson B., Ingason A., Sigfusson S., Hardardottir H., Harvey R.P., Brunner D., Mutel V., Gonzalo A., Lesne G., Sainz J., Obannesson G., Andresson T., Gudhjartsson D., Manolescu A., Erigge M.L., Gurney M.E., Kong A., Gulcher J.R., Petursson H., Stefansson K.;

**Neuregulin I and Susceptibility to Schizophrenia.";

**A Missen M. Genet. 71:0-0(2002)

**A Missen M. Genet. 71:0-0(2002)

**Chizophrenia.";

**A Missen M. Genet. 71:0-0(2002)

**A Missen M. Genet. 71:0-0(200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSLV
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                                                                                                                                                                           Craniata, Vertebrata, Eutelo
Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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Pred. No. 2.2e-106;
3; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO1089; NEUREGULIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS50026; EGF_3; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 462 AA; 50848 MW; 8
                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.2%;
94.4%;
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Pfam; PF02158; Neuregulin; 1.
01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Neuregulin 1 isoform ndf43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.4
Matches 405; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 1.
Pfam; PF00047; iq: 1.
                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            PubMed=12145742;
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61 WFKNGNELNFKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGNDSASANITI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 VESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 CVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEELYQKRVL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 KGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEYSSLRFK
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Oyotcolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AA; 42980 MW; C183EE80927443F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SM00408; IGC2; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01086; EGF 2; 1.
PROSITE; PS50036; IG_IKE; 1.
PROSITE; PS50835; IG_IKE; 1.
BGF-11ke domain.
NON_TER 1
NON_TER 394 AA; 42980 MW;
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SMART; SM00181; EGF; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                   YRDSPHSERY 429
                                                                                                                                                                                                                            414 YRDSPHSERH 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6TGK9;
                                                                                                                                                                                                                                                                                                                                      RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEELYOKRVLTITGICIALLVVGIMCVVAYCKTKKORKKLHDRLROSLRSERNNMMNIAN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 AEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRQKLHDRLLQSLRSERNNMVNIAN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Resoriceus auretus (Golden nameser).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Velasco J.A., Feijoo E., Avila M.A., Notario V.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 EGF-like domain.
EMBL: (U96612; AAB71812.1; -.
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                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0005102; P:rembryonic development; IEA.
InterPro; IPR006209; EGF 1.
InterPro; IPR006209; EGF 1.
InterPro; IPR006210; IEGF.
InterPro; IPR00110; Ig-11ke.
IPR01118; EGF; I.
IPR05ITE; PS0012; EGF 1; I.
IPR05ITE; PS0012; EGF 2; I.
IPR05ITE; PS0012; EGF 2; I.
IPR05ITE; PS00186; EGF 2; I.
                                                                                                                                                                                                                                   461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                PRELIMINARY;
RDSPHSERY 429
                                        |||||||||
RDSPHSERH 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus
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Gaps

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370 SESHSVIVMSSVENSRHSSPIGGPRGRLNGTGGPRECNS 408
                                                  356 SESHSVIMMSSVENSRHSSPTGGPRGRLNGLGGPRECNS 394
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Search completed: April 12, 2005, 14:33:51 Job time : 187 secs

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April 12, 2005, 14:26:42 ; Search time 48 Seconds (without alignments) 1292.913 Million cell updates/sec Run on:

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1 MSERKEGRGKGKGKKKERGS.....QEEIQARLSSVIANQDPIAV 645 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	herequip, splice	ρ	herequlin precurso	neu differentiatio	neu differentiatio	neu differentiatio	acetylcholine rece	neu differentiatio	neu differentiatio	herequlin precurso	glial growth facto	neu differentiatio	ErbB kinase activa	ErbB kinase activa	ErbB kinase activa	glial growth facto	neu differentiatio	heregulin isoform	neu differentiatio	sensory/motor neur	neuregulin-3 [impo	ErbB kinase activa	protein T6D22.14 [	hypothetical prote		neural cell adhesi	hypothetical prote	늄	hypothetical prote
SUMMARIES		1	C43273	A43273	161718	161722	161719	A45769	I38404	138403	D43273	832359	A56210	JC5701	JC5700	JC5702	S32357	138408	862676	138405	A56943	T44447	PC4415	D86215	T34513	B42680	IJCHNL	T13594	T13893	T33100
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	Query Match Length		637	640	636	662	639	602	462	350	241	241	230	898	850	860	422	175	125	125	296	713	57	2254	3507	734	1091	1891	1920	1510
d	Query Match	9	98.0	95.7	91.6	91.4	89.0	75.5	62.3	52.3	35.3	32.8	31.6	30.7	29.7	29.6	24.7		16.3		10.5		5.5	5.4	5.3	5.1	5.1	5.1	5.0	4.8
	Score		3280	3202.5	3066.5	3058.5	2980	2526.5	2086.5	1751.5	1183	1098	1059	1028	993	992	827	788	545.5	485	351	334.5	182.5	181	179	172	171	170	169	191
	Result No.	1	7	٣	4	S	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		26	27		29

probable serine/th protein UNC-89 - C	hypothetical prote MSB2 protein - yea probable villin 2	elastic titin - hu microtubule-associ	neural cell adhesi BUD3 protein - yea	carbon catabolite hypothetical prote	nucleolar phosphop mycelial surface a	hypothetical prote regulatory protein	serine-rich protei
T18611 T29757	T16201 S25370 E84845	I38346 T13564	JN0635 S74285	S70704 T24008	138073 T17415	E86185 S61112	T39903
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1192	279 1306 955	7962 5327	1092	409	699 1203	402 844	534
8. C. I	4.4 7.6 7.6	4. 4. 2. 7.	4. 4. 7. 1.	4.5	4 4 4. 4.	4 4 4. 4.	4.4
159	156.5 155.5 151.5	151.5 151	150 149.5	149 149	147.5 147	146.5	146
30	3 3 3	35 36	37	39	4142	443	45

## ALIGNMENTS

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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Mono sapiens (man)
Airitle: Identification of herequlin, a specific activator of pl85 (erbB2).
Airitle: Identification of herequlin, a specific activator of pl85 (erbB2).
Airitle: Identification of herequlin, a specific activator of pl85 (erbB2).
Airitle: Identification of herequlin, a specific activator of pl85 (erbB2).
Airitle: Multiplication of herequlin, a specific activator of pl85 (erbB2).
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A;Btatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule 'type: mRNA
A;Molecule 'type: mRNA
A;Residues: 'A', 95-418,'F', 420-645 <RES>
A;Cross-references: EMBL:U02328; NID:g408406; PIDN:AAA19953.1; PID:g408407
C;Genetics:
A;Gene GDB:HGL
A;Cross-references: GDB:132656; OMIM:142445
A;Gene: GDB:HGL
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
C;Keywords: alternative splicing
F;182-221/Domain: EGF homology <EGF>
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99.8%; Pred. No. 1.3e-183;
tive 1; Mismatches 0;
B43273
heregulin, splice form beta 1 - human
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Best Local Similarity
Matches 644; Conserv
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AACESQUIN precursor, splice form alpha - human
NyAlternate names: breast cancer cell differentiation factor p45; Neu differentiation fa
C;Species: Homo sapiens (man)
C;Date: 31-Dec.1993 #sequence_revision 31-Dec.1993 #text_change 08-Sep-2002
C;Accession: A43273; A48498; A38155
C;Accession: A43273; A48498; A38155
C;Accession: A43273; A84498; MX.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansur, Science 256; 1205-1210, 1992
A;Title: Identification of heregulin, a specific activator of p185(erbB2).
A;Accession: A43273; MUID:92271253; PMID:1350381
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Accession: A43273
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Accession: A43273
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Accession: A43273
A;Status: nucleic acid sequence extracted from NUED backbone (NUEDF:103250)
A;Accession: A6400
A;Accession: A6400
A;Accession: A4400
A;Accession
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PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
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                                                                                        KCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLG1EFMEA
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C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
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A;Gene: GDB:HGL
A;Cross-references: GDB:132656; OMIM:142445
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: To bec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Sep-2002
CiAccession: C43373; I38407
Sicance 256, 1205-1210, 1992
A; Reference number: A43273; MUID:92271253; PMID:1350381
A; Reference number: A43273; MUID:92271253; PMID:1350381
A; Residues: Drealiminary; nucleic acid sequence not shown; not compared with conceptual trates and sequence not shown; not compared with conceptual trates and sequence not shown; not compared with conceptual trates are sequenced by the sminary; nucleic acid sequence not shown; not compared with conceptual trates are sequenced by the sminary; nucleic acid sequence not shown; not compared with conceptual trates are sequenced by the sminary; nucleic acid sequence not shown; not compared with a sequence number: A56210; MUID:94158863; PMID:7509448
A; Reference number: A56210; MUID:94158863; PMID:7509448
A; References: EMBL: U02329; NID:94108408; PIDN:AA19954.1; PID:9408409
A; Cross-references: EMBL: U02329; NID:940408; PIDN:AA19954.1; PID:9408409
A; Ganetion: Bp22-8p11
C; Superfamily: human heregulin; EGF homology; immunoglobulin homology
C; Superfamily: human heregulin; EGF homology; immunoglobulin homology
C; Reywords: alternative splicing
F; 182-221/Domain: EGF homology cEGF>
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C43273
heregulin precursor, splice form beta-2 - human
C;Species: Homo sapiens (man)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 08-Sep-2002
                                     241 BELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANG
                                                                                                                                              PHHPNPPPENVQLVVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
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                                                                                                               PHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSW
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 161722
R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M., Mol. Cell. Biol. 14, 1909-1919; J. 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa;Reference number: A56210; MUID:94158863; PMID:7509448
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Ressidues: 1-662 cRES>
A;Cross-references: UNIPROT:P43322; EMBL:U02322; NID:g408394; PIDN:AAA19947.1; PID:g4082
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
F;182-221/Domain: EGF homology cEGF>
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                   A,Molecule type: mRNA
A,Residues: 1-298,386,'V',388,'TR',391 <RE3>
A,Cross-references: EMBL:U02320; NID:g408390; PIDN:AAA19945.1; PID:g408391
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
F;182-221/Domain: EGF homology <EGF>
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                                                                                                                                                          91.6%; Score 3066.5; DB 2; Length 636; 91.6%; Pred. No. 8e-168; ive 22; Mismatches 23; Indels 9;
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Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 161718; 161720
R;Wen, D: Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;
Mol. Cell. Biol. 14, 1909-1919, 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Residues: I-636 cRES-
A;Ccession: I61728
A;Accession: I61721
A;Rattus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: I61721
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: I61721
A;Residues: I-444,'A',446-636 cRE2-
A;Ccoss-references: EMBL:U02321; NID:9408392; PIDN:AAA19946.1; PID:9408393
A;Accession: I61720
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                                                                  DB 2;
                                                                Score 3202.5; DB 2;
Pred. No. 1.4e-175;
1; Mismatches 15;
C, Keywords: alternative splicing; glycoprotein F;182-221/Domain: EGF homology <EGF>
                                                                Query Match
Best Local Similarity 96.7%;
Matches 624; Conservative
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Cross-references: EMBL:U02323; NID:g408396; PIDN:AAA19948.1; PID:g408397
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neu differentiation factor - rat
neu differentiation factor - rat
neu differentiation factor - rat
C;Specis Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence revision 29-May-1998 #text change 09-Jul-2004
C;Accession: I61719; I61723; \(\overline{161717}\); I61724; A38\(\overline{161719}\); I61729; I61729; I61727; I61724; A38\(\overline{161719}\); I61719; I61729; I61729; I61719; I61729; I61719; I61729; I61719; If1719; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMIVSMPSVAVSPFVEEERPLILVIPPRLREKKYDHHPQQLNSPHNPAHQSTSLPPSPL
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                                                                                               MSERKEGRGKGKKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS
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                                                                                                                                                                                                                                                                                                                                                                                                                               -----KHLGIEFMEAEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDR
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                   Length 662
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                                                           Indels
                   DB 2;
                                                           28;
                                      Pred. No. 2.4e-167;
25; Mismatches 28;
                   Score 3058.5;
Pred. No. 2.4e
                 91.4%;
89.1%;
                                    Best Local Similarity 89.1%
Matches 591; Conservative
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A; Residues: 1-422, "HK."
A; Accession: 15117
A; Accession: 15117
A; Accession: 15117
A; Cross-references: EMBL:U02316; NID:9408382; PIDN:AAA19941.1; PID:9408383
A; Accession: 15117
A; Accession: 15117
A; Molecule type: mRNA
A; Residues: 1-422, "H', "NL', 637-638, "ELRRNKANRENCONOLOLSATHLRPSSITHLGFIL' «RE4>
A; Cross-references: EMBL:U02317; NID:9408384; PIDN:AAA19942.1; PID:9408385
A; Accession: 151724
A; Cross-references: EMBL:U02317; NID:9408384; PIDN:AAA19942.1; PID:9408385
A; Accession: 151724
A; Molecule type: mRNA
A; Residues: 1-422 «RE5>
A; Cross-references: EMBL:U02324; NID:9408398; PIDN:AAA19949.1; PID:9408399
R; Wen, D.; Peles, E.; Cupples, R.; Suggs, S.V.; Bacus, S.S.; Luo, Y.; Trail, G.; Hu, S.; Cell 69, 559-572, 1992
A; Title: Neu differentiation factor: a transmembrane glycoprotein containing an EGF dome A; Reference number: A38220; MUID:92257596; PMID:1349853
A; Accession: A38220
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-422 «WEN>
A; Note: sequence extracted from NCBI backbone (NCBIN:101767, NCBIP:101768)
C; Superfamily: human heregulin; EGF homology; immunoglobulin homology 180 239 359 539 593 120 120 180 234 299 294 354 419 413 479 473 533 9 9 DSASANITIVESNEFITGMPASTETAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLI KCAEKEKTFCVNGGECFTVKDLSNPSRYLCKCQPGFTGARCTENV-----PMKVQTQEK GPHHPNPPPENVOLVNOVVSKNVISSEHIVEREVETSFSTSHYTSTAHHSTTVTOTPSHS WSNGHTESVISESNSVIMMSSVENSRHSSPAGGPRGRLHGIGGPRD-NSFLRHARETPDS ERPLILVTPPRIREKKYDHHPQQLNSFHHNPAHQSTSLPPSPLRIVEDEEYETTQEYESV SEYSSLRFKWFKNGNELNFKNKPENIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN KCAEKEKTFCVNGGECFWVKDLSNPSRYLCKCPNBFTGDRCQNYVMASFYKHLGIEFME-AEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMNIAN AEELYQKRVLTITGICIALLVVGIMCVVAYCKTKKQRQKLHDRLRQSLRSERSNLVNIAN GPHHPNPPPENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHS 414 YRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSVAVSPFVEE **ERPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDSNSLPASPLRIVEDEEYETTQEYEPA** QEPVKKLANSRRAKRTKPNGHIANRLEVDSNTSSQSSNSESETEDERVGEDTPFLGIQNP MSERKEGRGKGKGKKKERGSGKKPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETS 1 MSERKEGRGKGKKKKDRGSRGKPGPAEGDPSPALPPRLKEMKSQESAAGSKLVLRCETS SEYSSLRFKWFKNGNELNRKNKPQNIKIQKKPGKSELRINKASLADSGEYMCKVISKLGN DSASANITIVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLV WSNGHTESILSESHSVIVMSSVENSRHSSPTGGPRGRLNGTGGPRECNSFLRHARETPDS YRDSPHSERYVSAMTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSMAVSPFMEE Gaps .; 8 Length 639; 645 Indels LAASLEATPAFRLADSRTNPAGRFSTQEEIQARLSSVIANQDPIAV Query Match

89.0%; Score 2980; DB 2; 1
Best Local Similarity 89.6%; Pred. No. 7e-163;
Matches 579; Conservative 25; Mismatches 34; A;Accession: 161716 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA

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C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: 138403

C;Accession: 138403

S;Accession: 138403

Mol. Cell. Biol. 14, 1909-1919, 1994

A;Title: Structural and functional aspects of the multiplicity of Neu differentiation f

A;Teference number: A56210; MUID: 94158863; PMID: 7509448

A;Accession: 138403

A;Accession: 138403

A;Accession: 138403

A;Accession: 138403

A;Accession: 138403

A;Residues: 1-350 cRES

A;Accessive: EMES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.3%; Score 2086.5; DB 2; Length Best Local Similarity 94.6%; Pred. No. 5.2e-112; Matches 406; Conservative 3; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                            C; Accession: A45769
K; Falls, D.L.; Rosen, K.M.; Corfas, G.; Lane, W.S.; Fischbach, G.D.
Cell 72, 801-815, 1993
A; Title: ARIA, a protein that stimulates acetylcholine receptor synthesis, is a member c A; Reference number: A45769; MUD: 93201602; PMID: 8453670
A; Accession: A57569
A; Accession: A57569
A; Residues: preliminary
A; Molecule type: mRNA; protein
A; Residues: 1-602 < FAL>
A; Residues: 1-602 < FAL>
A; Cross-references: UNIPROT: Q05199; GB: L11264; NID: 9212603; PIDN: AA449037.1; PID: 9212604
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIN: 127787, NCBIP: 127788)
C; Superfamily: human heregulin; EGF homology; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ATSTSTTGTSHLTKCDIKQKAFCVNGGECYMVKDLP 162
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                                                                                                                                                                                                                                 C;Spécies: Gallus gallus (chicken)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANGPHHPNPPPENVQLVNQYVSKNVI
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            639
    LAASLEVAPAFRLAESRTNPAGRFSTQEELQARLSSVIANQDPIAV
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les, I.; Davis, J. B.; Henan, J.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; Hen les, I.; Davis, J.B.; Henan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M. Nature 362, 312-318, 1993
A;Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in the n. A;Reference number: S32359
A;Accession: S32359
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-241
A;Residues: 1-241
A;Residues: 1-241
A;Residues: UNIPROT:007112; GB:L12259; NID:g289413; PIDN:AAA30540.1; PID:g289414!
F;182-221/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 02-011-1996 #sequence_revision 02-011-1996 #text_change 08-Sep-2002
C;Accession: A56210
C;Accession: A56210
R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;
Nol. Cell. Biol. 14, 1909-1919, 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fanty. Reference number: A56210; MUID:94158863; PMID:7509448
A;Recession: A56210
A;Accession: A56210
A;Accession: A56210
A;Accession: Robert anshared from GB/EMBL/DDBJ
A;Residuse: 1-230 - RES>
A;Cross-references: EMEL:U02315; NID:9408380; PIDN:AAA19940.1; PID:9408381
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
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                                                                                                                                                                                                  glial growth factor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
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Pred. No. 6.9e-56;
9; Mismatches 10;
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Pred. No. 1.1e-53;
4; Mismatches 10;
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llarity 91.7%;
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Matches 205; Conservative
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Best Local Simi
Matches 211;
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                                 ITGICIALLVVGIMCVVAYCKTKKQRKKLHDRLRQSLRSERNNMMIANGPHHPNPPPEN
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Best Local Simil
Matches 229; C
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OY 132 SNEITIGNPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFCV 19 Db 121 SNEITIGNPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKTFCV 19 Db 121 SNEITIGNPASTEGAYVSSESPIRISVSTPGANTSSSTSTSTTGTSHLVKCAEKEKTFCV 19	0 Qy 515 1 Db 706	ASLPASPLRIVEDEEYETTQEYEPAQEPVKKLANSRAKRTK 556 
192 NGGECFWYKDLSNFSRYLCKCPNEFTGDRCQNYWASFY 230	AQ QQ	557 PNGHIANRLEVDSNISSOSSNSESETEDERVGEDTPFLGIQNPL-AASL 604 
RESULT 13	Qy 605 EATPAFRLADSRT ::	IN 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
UCS/DB Kinase activator alphal, brain and thymus - rat C;Species: Rattus norvegicus (Norway rat) C;Bate: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 09-Jul-2004 C;Accession: JC5701; PC4411 R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa	T.; Miyag	pha, brain and thymus - human (man)
J. Biochem. 122, 675-680, 1997 A;Title: A novel brain-derived member of the epidermal growth factor family A;Reference number. JC5700; MUID:98006324; PMID:9348101 A;Accession: JC5701 A;Molecule type: mRNA	hat interac	<pre>puence_revision 25-Nov-1997 #text_change 09-Jul-2004 awa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyac p. 1997 # The enidermal growth factor family that interactions</pre>
A; Residues: 1-868 <hig> A; Cross-references: UNIPROT:035569; DDBJ:D89995; NID:g2605629; PIDN:BAA23346 A; Accession: PC4411 A; Molecule type: protein</hig>	1; PID:g260 A;Reference number: JCS A;Accession: JCS700 A;Status: nucleic acid & A;Molecule type: mRNA	00; MUID:98006324; PMID:9348101
A, Restudes: 128-128 - ALZ cell A, Experimental source: PC-12 cell C; Comment: This protein is a member of the epidermal growth factor family. It is a tring the differentiation of MDA-MB-453 cells. C; Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; P; 361-397/Domain: EGF homology < RGPs.	functic	A;Cross-references: UNIPROT:014511; DDBJ:AB005060; NID:g2626738; PIDN:BAA23417.1; PID:g. A;Cross-references: UNIPROT:014511; DDBJ:AB005060; NID:g2626738; PIDN:BAA23417.1; PID:g. A;Experimental source: SK-NSH cell C;Comment: This protein is a member of the epidermal growth factor family. It is functic ating the differentiation of MDA-MB-453 cells. C;Superfamily: human ErbB kinase activator alpha, brain and thymus; EGF homology; immunc
Query Match 30.7%; Score 1028; DB 2; Length 868; Best Local Similarity 37.7%; Pred. No. 3.4e-51; Matches 254; Conservative 97; Mismatches 188; Indels 134; Gaps	C.Keywords: glycoprotein F.258-311/Domain: 19-11) F.345-381/Domain: EGF h: F.346-381/Domain: EGF h:	e #status predicted <igl> mology <egf> ke #status predicted <egf2></egf2></egf></igl>
OY 11 GKGKKKERGSGKKPESAAGSQSPALPPOLKEMKSQESAAGSKLVLRCETSSEYSSLRFKW 70	w	<pre>1ce: carbohydrate (Asn) (covalent) #status predicted 29.7%; Score 993; DB 2; Length 850; 37.1%; Pred: No. 3.3e-49;</pre>
Qy 71 FKNGNELNRKNKPQNIKIQKKPCKSELRINKASLADSGEYMCKVISKLGNDSASANIT 128	Oy 11	
Qy 129 IVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTSTGTSHLVKCAEKEKT 181	8 0 00 7	
QY 189 FCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVMASFYKHLGIEFMEAEE 242	Db 271 Qy 129	SRLÇFNKVKVEDAGEYVCEAENILGKDTVRGRL- RISVSTEGANTSSSTSTSTTGTSHLVKCAEKEKT  :
QY         243 LYQKRVLTITGICIALLVVGIMCVVAXCKTKKQRKKLHDRLRQSLRSERNNMMNIANGH 302           Db         425 LYQKRVLTITGICVALLVVGIVCVVAXCKTKKQRRQMHHLRQNMCPAHQN-RSLANGPS 483	Db 327	
OY 303 HDNPPPBNVQLVNQYVSRAVISSEHIVBREAETSFSTSHYTSTAHKSTTVTQTPS 357	0y 249	
QY 358 HSWSNGHTESILSESHGVIVMSSVENSRHSSPT-GGPRGRLNGTGGPRECNSFLRHARET 416	00 AO	
Qy 417 PDSYRDSPHSERYVSAWTTPARMSPVDFHTPSSPKSPPSEMSPPVSSMTVSMPSM 471	DD 466 Qy 364	
Qy 472 A-VSPEWEBERPLLLVTPPRLREKKFDHHPQQFSSFHHNPAHDS 514	DD 525	525 KSESLITSDSQSGIMLSSVGTSKCNSPACVEARARRAAATNLEERRRATAPPYHDSV 580 418 DSYRDSPHSERYVSAMTTPARMSPVDFHIPSSPKSPPSEMSPPVSSMTVSMPSMA-VSPP 476 

309 ENVQLVNQYVSKNVISSEHIVEREAETSFSTSHYTSTAHHSTTVTQTPSHSWSNG   :   :	OY 515NSLPASPERIATORIZEAGEPYKILANSKRAKRYKNGHIA 562	Search completed: April 12, 2005, 14:42:49 Job time : 50 secs	
Db 581 DSLRDSPHSERYVSALTTPARLSPVDFHYSLATQVPTFEITSPNSAHAVSLPPAAPISYR 640  Qy 477 MEEBRPLLLVTPPRLREKKFDHHP	RESULT 15 JC5702 ErbB kinase activator alpha2a, brain and thymus - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: S-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 09-Jul-2004 C;Accession: JC5702; PG4417 R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Miyag J. Biochem. 122, 675-680, 1997 A;Title: A novel brain-derived member of the epidermal growth factor family that interactive the number; JC5700; MUID:98006324; PMID:9348101	A,Status: nucleic acid sequence not shown A,Status: nucleic acid sequence not shown A,Status: nucleic acid sequence not shown A,Molecule type: mRNA A,Residues: 1-860 <-HIG> A,Croserreferences: UNIPROT:035569; DDBJ:D89996; NID:g2605631; PIDN:BAA23345.1; PID:g260 A,Experimental source: PC-12 cell A,Accession: PC4417 A,Status: nucleic acid sequence not shown A,Molecule type: mRNA A,Residues: 'F',212-213,223-860 <-HIZ> A,Croserreferences: DDBJ:ABB001576; NID:g2605478; PIDN:BAA23348.1; PID:g2605479 A,Experimental source: PC-12 cell C,Comment: This protein is a member of the epidermal growth factor family. It is function ating the differentiation of MDA-MB-453 cells. C,Superfamily: human ErDB kinase activator alpha, brain and thymus; EGF homology; immunc C,Keywords: glycoprotein F;274-327/Domain: Ig-like #status predicted <igl>F;361-397/Domain: EGF homology <egf>F;361-397/Domain: BGF homology <egf>F;361-397/Domain: BGF homology <egf>F;163,294,467/Binding site: carbohydrate (Asn) (covalent) #status predicted</egf></egf></egf></igl>	Query Match         29.6%;         Score 992;         DB 2;         Length 860;           Best Local Similarity         37.2%;         Pred. No. 3.8e-49;         Indels 130;         Gaps 21;           QY         11 GKGKKKERGSGKRPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEYSSLRFKW         70         11 GKGKKKERGSGKRPESAAGSQSPALPPQLKEMKSQESAAGSKLVLRCETSSEYSSLRFKW         70           Db         234 GKNIKKEVGKILCTDCATRPKLKKWKSQTGEVGEKGSLKCEAAAGNPQPSTRW         286           QY         71 FKNGNELNRKNKPQNIKIQKKPGKSELRINKASIADSGEYNCKYSIGNDSASANIT         128           Db         287 FKDGKELNRSRDIRIKYGNGRKNSRLOPNKVKVEDAGEYVCEAENILGKDTVRGRLH         343           QY         129 IVESNEIITGMPASTEGAYVSSESPIRISVSTEGANTSSSTSTTGTSHLVKCAEKEKT         186           Db         344 V